

94	6	5.9	418	4	075066	KIAA0478 PROTEIN.	1.80e+01	167	6	5.9	838	10	049372	HYPOTHETICAL 92.4 KD P	1.80e+01
95	6	5.9	420	14	067008	POLYPROTEIN PRECURSOR	1.80e+01	168	6	5.9	857	14	073289	ENVELOPE GLYCOPROTEIN.	1.80e+01
96	6	5.9	420	2	085656	SERINE HYDROXYMETHYLTR	1.80e+01	169	6	5.9	869	4	000513	GUANINE NUCLEOTIDE EXC	1.80e+01
97	6	5.9	425	2	053615	SERINE HYDROXYMETHYLTR	1.80e+01	170	6	5.9	878	4	09Y5C2	PROTODADHERIN GAMMA C5	1.80e+01
98	6	5.9	426	2	053411	SERINE HYDROXYMETHYLTR	1.80e+01	171	6	5.9	879	5	09XZ14	HYPOTHETICAL 100.1 KD	1.80e+01
99	6	5.9	426	2	09X794	PUTATIVE SERINE HYDROX	1.80e+01	172	6	5.9	882	5	021567	M28-4 PROTEIN.	1.80e+01
100	6	5.9	434	2	052963	CHEMOTAXIS MOTC PROTEI	1.80e+01	173	6	5.9	890	14	012936	PUTATIVE DNA-DIRECTED	1.80e+01
101	6	5.9	434	2	054327	TOXIN DEGRADING PROTEA	1.80e+01	174	6	5.9	912	4	092888	GUANINE NUCLEOTIDE EXC	1.80e+01
102	6	5.9	437	11	035249	CD44 (FRAGMENT).	1.80e+01	175	6	5.9	919	11	092116	LSC PROTEIN.	1.80e+01
103	6	5.9	440	2	007120	SURFACE LAYER PROTEIN.	1.80e+01	176	6	5.9	919	11	061210	LYMPHOID BLAST CRISIS	1.80e+01
104	6	5.9	445	5	09XYW4	COP9 COMPLEX HOMOLOG S	1.80e+01	177	6	5.9	944	4	09Y5F6	PROTODADHERIN GAMMA C5	1.80e+01
105	6	5.9	446	1	025791	PHOSPHOMANNOMUTASE (PM	1.80e+01	178	6	5.9	967	5	018281	SIMILARITY TO VERY-LON	1.80e+01
106	6	5.9	448	2	034824	YBBT PROTEIN.	1.80e+01	179	6	5.9	968	10	081357	PHOSPHENOLPYRUVATE CA	1.80e+01
107	6	5.9	448	2	087090	YBBT PROTEIN.	1.80e+01	180	6	5.9	1007	11	062641	GLUTAMATE RECEPTOR DEL	1.80e+01
108	6	5.9	455	8	003658	RIBULOSE BISPHOSPHATE	1.80e+01	181	6	5.9	1007	11	061625	GLUTAMATE RECEPTOR CHA	1.80e+01
109	6	5.9	456	2	048508	SB-PROTEIN PRECURSOR.	1.80e+01	182	6	5.9	1007	4	043424	GLUTAMATE RECEPTOR DEL	1.80e+01
110	6	5.9	457	10	080701	F8K4.15 PROTEIN.	1.80e+01	183	6	5.9	1008	11	063226	GLUTAMATE RECEPTOR SUB	1.80e+01
111	6	5.9	460	14	09NSO6	HYPOTHETICAL 51.1 KD P	1.80e+01	184	6	5.9	1088	11	0921X1	GLUT4 VESICLE PROTEIN.	1.80e+01
112	6	5.9	466	8	098743	RIBULOSE BISPHOSPHATE	1.80e+01	185	6	5.9	1099	5	090731	B0365.1 PROTEIN.	1.80e+01
113	6	5.9	475	8	09XOC1	RIBULOSE BISPHOSPHATE	1.80e+01	186	6	5.9	1149	10	082331	PUTATIVE REVERSE TRANS	1.80e+01
114	6	5.9	475	8	09XOC2	RIBULOSE BISPHOSPHATE	1.80e+01	187	6	5.9	1192	5	046072	COSMID 30B8.	1.80e+01
115	6	5.9	475	8	092255	RIBULOSE BISPHOSPHATE	1.80e+01	188	6	5.9	1201	5	024240	ACTIN BINDING PROTEIN.	1.80e+01
116	6	5.9	476	8	099255	CYTOCHROME C OXIDASE S	1.80e+01	189	6	5.9	1231	11	055092	SERINE/THREONINE KINASE	1.80e+01
117	6	5.9	476	8	099252	CYTOCHROME C OXIDASE S	1.80e+01	190	6	5.9	1262	3	013327	PROTEIN PHOSPHATASE SS	1.80e+01
118	6	5.9	477	8	062944	RIBULOSE BISPHOSPHATE	1.80e+01	191	6	5.9	1413	10	092VW0	PUTATIVE RETROTRANSPOS	1.80e+01
119	6	5.9	477	5	026218	CYTOCHROME C OXIDASE S	1.80e+01	192	6	5.9	1426	3	078577	ATP-BINDING CASSETTE M	1.80e+01
120	6	5.9	478	8	063176	CYTOCHROME C OXIDASE S	1.80e+01	193	6	5.9	1490	5	001319	F02E9.4 PROTEIN.	1.80e+01
121	6	5.9	483	14	09NAU1	HEXON PROTEIN (FRAGMEN	1.80e+01	194	6	5.9	1503	10	081283	T14F8.24 PROTEIN.	1.80e+01
122	6	5.9	485	2	09WXP2	HYPOTHETICAL 55.6 KD P	1.80e+01	195	6	5.9	1522	4	015085	KIAA0380.	1.80e+01
123	6	5.9	490	2	085997	SEMIALDEHYDE DEHYDROGE	1.80e+01	196	6	5.9	1539	4	015078	KIAA0373.	1.80e+01
124	6	5.9	504	14	074117	GP105 (FRAGMENT).	1.80e+01	197	6	5.9	1676	10	023332	CENTROMERE PROTEIN HOM	1.80e+01
125	6	5.9	507	14	074115	GP105 (FRAGMENT).	1.80e+01	198	6	5.9	1679	5	026607	SURFACE PROTEIN (FRAGM	1.80e+01
126	6	5.9	508	14	074118	GP105 (FRAGMENT).	1.80e+01	199	6	5.9	1732	10	023576	DNA CHROMOSOME 4, ESSA	1.80e+01
127	6	5.9	508	14	074116	GP105 (FRAGMENT).	1.80e+01	200	6	5.9	1829	4	015015	KIAA0296.	1.80e+01
128	6	5.9	512	2	008251	LIPOPROTEIN.	1.80e+01	201	6	5.9	1890	10	049528	GENE 11-1 PROTEIN - LI	1.80e+01
129	6	5.9	519	5	046018	ZK570.1 PROTEIN.	1.80e+01	202	6	5.9	1992	13	004834	NONMUSCLE MYOSIN HEAVY	1.80e+01
130	6	5.9	549	4	099475	KM-102-DERIVED REDUCTA	1.80e+01	203	6	5.9	2030	5	061850	F55F10.2 PROTEIN.	1.80e+01
131	6	5.9	551	2	071732	HYPOTHETICAL 61.4 KD P	1.80e+01	204	6	5.9	2160	5	017709	H05L14.2 PROTEIN.	1.80e+01
132	6	5.9	559	5	077472	LEUCINE-RICH REPEAT PR	1.80e+01	205	6	5.9	2253	4	095850	POLYCYSTIC KIDNEY DISE	1.80e+01
133	6	5.9	561	2	033131	HYPOTHETICAL 61.8 KD P	1.80e+01	206	6	5.9	2510	5	019482	F1589.7 PROTEIN.	1.80e+01
134	6	5.9	565	2	051685	HYPOTHETICAL 65.7 KD P	1.80e+01	207	6	5.9	3262	5	027254	CPY GENE.	1.80e+01
135	6	5.9	568	2	0929G0	PREDICTED OMP.	1.80e+01	208	6	5.9	3726	5	027255	TRITHORAX PROTEIN TRX.	1.80e+01
136	6	5.9	568	3	09Y7M1	PUTATIVE OXALYL-COA DE	1.80e+01	209	6	5.9	3828	5	027255	PREDICTED TRITHORAX PR	1.80e+01
137	6	5.9	569	10	084506	T20F6.9 PROTEIN.	1.80e+01	210	6	5.9	37	14	090372	HAEMAGGLUTININ-NEURAM	1.80e+01
138	6	5.9	572	5	022875	AC7.2 PROTEIN.	1.80e+01	211	6	5.9	40	14	068321	E2/NS1 (FRAGMENT).	1.80e+01
139	6	5.9	577	5	024571	SOB PROTEIN.	1.80e+01	212	6	5.9	43	14	09YPD3	ENVELOPE PROTEIN (FRAG	1.80e+01
140	6	5.9	582	10	09XIW5	SIMILAR TO GLYCINE MAX	1.80e+01	213	6	5.9	46	14	079935	POL (FRAGMENT).	1.80e+01
141	6	5.9	586	3	094019	TRANSPORT PROTEIN.	1.80e+01	214	6	5.9	46	14	079935	REVERSE TRANSCRIPTASE	1.80e+01
142	6	5.9	586	9	084308	REPLICASE.	1.80e+01	215	6	5.9	46	14	082278	REVERSE TRANSCRIPTASE	1.80e+01
143	6	5.9	599	10	080528	F14J9.11 PROTEIN.	1.80e+01	216	6	5.9	46	14	082287	REVERSE TRANSCRIPTASE	1.80e+01
144	6	5.9	624	2	095626	METHYLATION ACCEPTING	1.80e+01	217	6	5.9	46	14	079934	POL (FRAGMENT).	1.80e+01
145	6	5.9	637	5	093512	F15D4.4 PROTEIN.	1.80e+01	218	6	5.9	46	14	079941	POL (FRAGMENT).	1.80e+01
146	6	5.9	638	1	026315	FEROUS IRON TRANSPORT	1.80e+01	219	6	5.9	46	14	079940	POL (FRAGMENT).	1.80e+01
147	6	5.9	640	5	09XWZ6	Y42A5A.2 PROTEIN.	1.80e+01	220	6	5.9	46	14	055266	POL POLYPROTEIN (FRAGM	1.80e+01
148	6	5.9	643	5	022886	SIMILARITY TO EGF-LIKE	1.80e+01	221	6	5.9	46	14	079935	POLYPROTEIN (FRAGMENT)	1.80e+01
149	6	5.9	674	11	035772	GROWTH POTENTIATING FA	1.80e+01	222	6	5.9	49	14	087344	ENVELOPE GLYCOPROTEIN	1.80e+01
150	6	5.9	676	5	045553	F53A2.8 PROTEIN (EC 3.	1.80e+01	223	6	5.9	70	14	087341	ENVELOPE GLYCOPROTEIN	1.80e+01
151	6	5.9	697	4	043167	KIAA0441.	1.80e+01	224	6	5.9	72	14	087341	FUSION PROTEIN (FRAGME	1.80e+01
152	6	5.9	700	2	072127	FLAGELLIN (FRAGMENT).	1.80e+01	225	6	5.9	72	14	087343	ENVELOPE GLYCOPROTEIN	1.80e+01
153	6	5.9	701	11	0921X5	GLUT4 VESICLE PROTEIN.	1.80e+01	226	6	5.9	73	14	087433	ENVELOPE GLYCOPROTEIN	1.80e+01
154	6	5.9	708	5	091954	ACETYLCHOLINESTERASE.	1.80e+01	227	6	5.9	76	13	090641	CAMP-DEPENDENT PROTEIN	1.80e+01
155	6	5.9	712	4	073557	DJ1163J1.3 (NOVEL PROT	1.80e+01	228	6	5.9	84	14	036993	FUSION PROTEIN (FRAGME	1.80e+01
156	6	5.9	720	1	091955	HYDROPEROXIDASE.	1.80e+01	229	6	5.9	84	14	036999	FUSION PROTEIN (FRAGME	1.80e+01
157	6	5.9	765	2	092LEB	PUTATIVE HYDANTOIN UTI	1.80e+01	230	6	5.9	89	5	096919	TC1-LIKE TRANSPOSASE (1.80e+01
158	6	5.9	765	2	025403	N-METHYLHYDANTOINASE.	1.80e+01	231	6	5.9	90	2	048880	HYPOTHETICAL 10.2 KD P	1.80e+01
159	6	5.9	775	4	060347	KIAA0608 PROTEIN (FRAG	1.80e+01	232	6	5.9	92	10	092TM9	PGP219.	1.80e+01
160	6	5.9	780	11	008779	CD44 PROTEIN.	1.80e+01	233	6	5.9	92	10	092TM9	PGP219.	1.80e+01
161	6	5.9	780	4	075157	KIAA0669 PROTEIN.	1.80e+01	234	6	5.9	93	13	013002	ZP3 HOMOLOG (FRAGMENT)	1.80e+01
162	6	5.9	808	10	092R56	RIBONUCLEOTIDE REDUCTA	1.80e+01	235	6	5.9	94	11	062507	COCHLEAR MRNA (CLONE 3	1.80e+01
163	6	5.9	808	10	092R57	RIBONUCLEOTIDE REDUCTA	1.80e+01	236	6	5.9	98	2	092J78	PUTATIVE.	1.80e+01
164	6	5.9	809	3	086693	CHROMOSOME XV READING	1.80e+01	237	6	5.9	107	3	005413	DNA FOR ORF'S FROM CHR	1.80e+01
165	6	5.9	810	3	002553	P53 ACTIVITY REGULATOR	1.80e+01	238	6	5.9	109	8	047626	CYTOCHROME B (FRAGMENT	1.80e+01
166	6	5.9	827	10	004578	SEQUENCE OF BAC F19K23	1.80e+01	239	6	5.9	110	10	023624	FPP1 PROTEIN.	1.80e+01

240	5	5.0	110	2	Q92863	HIT FAMILY HYDROLASE.	9.24e+02	313	5	5.0	212	2	Q25248	CONSERVED HYPOTHETICAL	9.24e+02
241	5	5.0	111	8	Q47623	CYTOCHROME B (FRAGMENT	9.24e+02	314	5	5.0	214	13	Q42134	'DNA TOPOISOMERASE IIB	9.24e+02
242	5	5.0	115	10	Q23759	UBIQUITIN PROTEIN.	9.24e+02	315	5	5.0	214	11	Q63177	PILQ	9.24e+02
243	5	5.0	116	14	Q82356	HTLV-II PROVIRUS POL G	9.24e+02	316	5	5.0	215	2	Q50970	T20D3.1 PROTEIN.	9.24e+02
244	5	5.0	116	14	Q82342	HTLV-II PROVIRUS POL G	9.24e+02	317	5	5.0	216	5	Q01253	MA56 PRECURSOR.	9.24e+02
245	5	5.0	118	11	Q95301	INTERPHOTORECEPTOR RET	9.24e+02	318	5	5.0	218	14	Q93J74	CHROMOSOME XII COSMID	9.24e+02
246	5	5.0	119	5	Q17424	PROBABLE THIOREDOLIN.	9.24e+02	319	5	5.0	220	3	Q05778	OMPA.	9.24e+02
247	5	5.0	123	14	Q9WA25	POLYPROTEIN (FRAGMENT)	9.24e+02	320	5	5.0	220	2	Q9XAX8	VSRC.	9.24e+02
248	5	5.0	123	14	Q9WP26	POLYPROTEIN (FRAGMENT)	9.24e+02	321	5	5.0	220	2	Q05415	D9509.18P.	9.24e+02
249	5	5.0	127	6	Q04209	THYROGLOBULIN (FRAGMENT)	9.24e+02	322	5	5.0	221	3	Q04178	LIGHT-HARVESTING COMPL	9.24e+02
250	5	5.0	128	8	Q35285	CYTOCHROME OXIDASE I (9.24e+02	323	5	5.0	221	8	Q36717	228AA LONG HYPOTHETICA	9.24e+02
251	5	5.0	129	1	Q9YFS8	HYPOTHETICAL 14.9 KD P	9.24e+02	324	5	5.0	228	1	Q59035	MRNA EXPRESSED IN CUCU	9.24e+02
252	5	5.0	129	2	Q73361	F36D1.7 PROTEIN.	9.24e+02	325	5	5.0	230	10	Q9XIV0	HYPOTHETICAL 24.5 KD P	9.24e+02
253	5	5.0	130	5	Q9XV43	FUSION PROTEIN (FRAGME	9.24e+02	326	5	5.0	231	2	Q58733	F35B12.3 PROTEIN.	9.24e+02
254	5	5.0	130	14	Q55668	FUSION PROTEIN (FRAGME	9.24e+02	327	5	5.0	231	1	Q58733	HYPOTHETICAL 26.3 KD P	9.24e+02
255	5	5.0	130	14	Q55666	FUSION PROTEIN (FRAGME	9.24e+02	328	5	5.0	232	5	Q20013	HYPOTHETICAL 26.4 KD P	9.24e+02
256	5	5.0	130	14	Q55674	FUSION PROTEIN (FRAGME	9.24e+02	329	5	5.0	232	10	Q65705	CARAMOYL-PHOSPHATE SY	9.24e+02
257	5	5.0	130	14	Q55674	FUSION PROTEIN (FRAGME	9.24e+02	330	5	5.0	233	13	Q42185	BIOTIN LIGASE BIRA HOM	9.24e+02
258	5	5.0	130	14	Q55672	FUSION PROTEIN (FRAGME	9.24e+02	331	5	5.0	235	1	Q73952	PAROTID SECRETORY PROT	9.24e+02
259	5	5.0	130	14	Q55681	FUSION PROTEIN (FRAGME	9.24e+02	332	5	5.0	235	11	Q63471	HYPOTHETICAL 26.3 KD P	9.24e+02
260	5	5.0	132	9	Q9XJP0	P12 (FRAGMENT).	9.24e+02	333	5	5.0	236	2	Q84313	MATRIX PROTEIN M1 (FRA	9.24e+02
261	5	5.0	134	14	Q39518	RNA DEPENDENT RNA POLY	9.24e+02	334	5	5.0	238	14	Q9WHX7	MALONATE DECARBOXYLASE	9.24e+02
262	5	5.0	135	10	Q64622	F19F24.12 PROTEIN.	9.24e+02	335	5	5.0	238	2	Q54417	PROLACTIN-LIKE PROTEIN	9.24e+02
263	5	5.0	138	13	Q9XGQ9	CADHERIN (FRAGMENT).	9.24e+02	336	5	5.0	238	11	Q08627	MATRIX PROTEIN M1 (FRA	9.24e+02
264	5	5.0	140	14	Q9WF47	FUSION GLYCOPROTEIN PR	9.24e+02	337	5	5.0	239	14	Q9WHX8	MATRIX PROTEIN M1 (FRA	9.24e+02
265	5	5.0	141	14	Q9WF48	FUSION GLYCOPROTEIN PR	9.24e+02	338	5	5.0	239	14	Q9WHY0	MATRIX PROTEIN M1 (FRA	9.24e+02
266	5	5.0	141	2	Q55934	SYCH.	9.24e+02	339	5	5.0	239	14	Q9WHY1	MATRIX PROTEIN M1 (FRA	9.24e+02
267	5	5.0	142	14	Q9WF48	FUSION GLYCOPROTEIN PR	9.24e+02	340	5	5.0	239	14	Q9WHX9	MATRIX PROTEIN M1 (FRA	9.24e+02
268	5	5.0	142	3	Q92425	MANGANESE-SUPEROXIDE D	9.24e+02	341	5	5.0	239	14	Q9WHY7	MATRIX PROTEIN M1 (FRA	9.24e+02
269	5	5.0	142	3	Q92424	MANGANESE-SUPEROXIDE D	9.24e+02	342	5	5.0	239	14	Q9WHY6	MATRIX PROTEIN M1 (FRA	9.24e+02
270	5	5.0	144	14	Q9WF40	FUSION GLYCOPROTEIN PR	9.24e+02	343	5	5.0	239	14	Q9WHY9	MATRIX PROTEIN M1 (FRA	9.24e+02
271	5	5.0	144	14	Q9WF40	MAJOR CAPSID PROTEIN L	9.24e+02	344	5	5.0	239	14	Q9WHY8	MATRIX PROTEIN M1 (FRA	9.24e+02
272	5	5.0	145	10	Q40431	PSI-H PRECURSOR.	9.24e+02	345	5	5.0	239	14	Q9WHY3	MATRIX PROTEIN M1 (FRA	9.24e+02
273	5	5.0	146	14	Q9NGF4	MAJOR CAPSID PROTEIN L	9.24e+02	346	5	5.0	239	14	Q9WHY4	MATRIX PROTEIN M1 (FRA	9.24e+02
274	5	5.0	149	10	Q65857	GLUTATHIONE S-TRANSFER	9.24e+02	347	5	5.0	241	2	Q67285	ALCOHOL DEHYDROGENASE.	9.24e+02
275	5	5.0	150	14	Q9WF37	FUSION GLYCOPROTEIN PR	9.24e+02	348	5	5.0	241	2	Q67285	POLYHEDRIN.	9.24e+02
276	5	5.0	151	14	Q9WF43	FUSION GLYCOPROTEIN PR	9.24e+02	349	5	5.0	242	2	Q05883	WATER CHANNEL PROTEIN	9.24e+02
277	5	5.0	151	14	Q9WF41	FUSION GLYCOPROTEIN PR	9.24e+02	350	5	5.0	245	14	Q9YMX2	14-3-3 PROTEIN	9.24e+02
278	5	5.0	151	14	Q9WF38	FUSION GLYCOPROTEIN PR	9.24e+02	351	5	5.0	248	10	Q9XF76	MATRIX PROTEIN M1 (FRA	9.24e+02
279	5	5.0	151	7	Q98204	MHC CLASS I (FRAGMENT)	9.24e+02	352	5	5.0	249	10	Q93787	MATRIX PROTEIN M1.	9.24e+02
280	5	5.0	153	14	Q9WF42	FUSION GLYCOPROTEIN PR	9.24e+02	353	5	5.0	250	14	Q9WHY2	MATRIX PROTEIN.	9.24e+02
281	5	5.0	154	14	Q9WF39	FUSION GLYCOPROTEIN PR	9.24e+02	354	5	5.0	252	14	Q9W9L6	MATRIX PROTEIN.	9.24e+02
282	5	5.0	154	14	Q9Y557	FUSION GLYCOPROTEIN PR	9.24e+02	355	5	5.0	252	14	Q9W8D8	MATRIX PROTEIN.	9.24e+02
283	5	5.0	154	14	Q84411	GENOME, PARTIAL SEQUE	9.24e+02	356	5	5.0	252	14	Q9W8D8	MATRIX PROTEIN 1.	9.24e+02
284	5	5.0	154	14	Q97659	ENVELOPE GLYCOPROTEIN	9.24e+02	357	5	5.0	252	14	Q9W8Z4	MATRIX PROTEIN 1.	9.24e+02
285	5	5.0	157	10	Q39338	OLEOSIN.	9.24e+02	358	5	5.0	252	14	Q9W8E6	MATRIX PROTEIN 1.	9.24e+02
286	5	5.0	164	5	Q01778	CODED FOR BY C. ELEGAN	9.24e+02	359	5	5.0	252	14	Q9W8Z6	MATRIX PROTEIN 1.	9.24e+02
287	5	5.0	164	10	Q38835	HYPOTHETICAL 17.7 KD P	9.24e+02	360	5	5.0	252	14	Q9W8C01	MATRIX PROTEIN 1.	9.24e+02
288	5	5.0	165	7	Q98207	MHC CLASS I (FRAGMENT)	9.24e+02	361	5	5.0	252	14	Q9W8C01	MATRIX PROTEIN 1.	9.24e+02
289	5	5.0	169	2	Q92C79	102 KBASES UNSTABLE RE	9.24e+02	362	5	5.0	252	14	Q9W8Y8	MATRIX PROTEIN 1.	9.24e+02
290	5	5.0	170	7	Q98210	MHC CLASS I (FRAGMENT)	9.24e+02	363	5	5.0	252	14	Q9W8Y8	MATRIX PROTEIN 1.	9.24e+02
291	5	5.0	171	1	Q27890	CONSERVED PROTEIN.	9.24e+02	364	5	5.0	252	14	Q9W8Y4	MATRIX PROTEIN 1.	9.24e+02
292	5	5.0	173	10	Q22257	HYPOTHETICAL PROTEIN.	9.24e+02	365	5	5.0	252	14	Q9W8Y4	MATRIX PROTEIN 1.	9.24e+02
293	5	5.0	176	14	Q9YPH1	TRIPLE-GENE-BLOCK THIR	9.24e+02	366	5	5.0	252	14	Q9W8C06	MATRIX PROTEIN 1.	9.24e+02
294	5	5.0	180	5	Q18997	D2089.2 PROTEIN.	9.24e+02	367	5	5.0	252	14	Q9W8Y0	MATRIX PROTEIN 1.	9.24e+02
295	5	5.0	181	2	Q68404	ALPHA HEMOLYSIN (FRAGM	9.24e+02	368	5	5.0	252	14	Q9W8Y0	MATRIX PROTEIN 1.	9.24e+02
296	5	5.0	181	2	Q68404	ALPHA HEMOLYSIN (FRAGM	9.24e+02	369	5	5.0	252	14	Q9W8Y0	MATRIX PROTEIN 1.	9.24e+02
297	5	5.0	182	3	Q93973	ALLERGEN (FRAGMENT).	9.24e+02	370	5	5.0	252	14	Q9W8Y5	MATRIX PROTEIN M1.	9.24e+02
298	5	5.0	183	10	Q64933	MADS BOX PROTEIN.	9.24e+02	371	5	5.0	252	14	Q9YIL2	M1 PROTEIN.	9.24e+02
299	5	5.0	189	14	Q90446	VIRION PROTEIN.	9.24e+02	372	5	5.0	252	14	Q9YIP63	M1 PROTEIN.	9.24e+02
300	5	5.0	189	14	Q90446	VIRION PROTEIN.	9.24e+02	373	5	5.0	252	14	Q9YIP63	MEMBRANE PROTEIN M1.	9.24e+02
301	5	5.0	193	5	Q76215	DENSE GRANULE PROTEIN	9.24e+02	374	5	5.0	252	14	Q89562	MEMBRANE PROTEIN M1.	9.24e+02
302	5	5.0	194	2	Q69747	IGAL PROTEASE (FRAGMEN	9.24e+02	375	5	5.0	252	14	Q67157	MATRIX PROTEIN.	9.24e+02
303	5	5.0	195	14	P89530	PUTATIVE COAT PROTEIN	9.24e+02	376	5	5.0	252	14	Q67152	MATRIX PROTEIN.	9.24e+02
304	5	5.0	200	2	Q9X6E9	PHENYLALANYL-TRNA-SYNT	9.24e+02	377	5	5.0	252	14	Q67161	MEMBRANE PROTEIN M1.	9.24e+02
305	5	5.0	202	14	Q95833	COAT PROTEIN.	9.24e+02	378	5	5.0	252	14	Q67147	MATRIX PROTEIN 1.	9.24e+02
306	5	5.0	202	14	Q65834	COAT PROTEIN.	9.24e+02	379	5	5.0	253	10	Q9Z5T8	TIC20.	9.24e+02
307	5	5.0	202	14	Q65840	COAT PROTEIN.	9.24e+02	380	5	5.0	254	5	Q62154	F11D11.5 PROTEIN.	9.24e+02
308	5	5.0	202	14	Q65839	COAT PROTEIN.	9.24e+02	381	5	5.0	256	14	Q9WM14	FUSION PROTEIN (FRAGME	9.24e+02
309	5	5.0	202	14	Q65841	COAT PROTEIN.	9.24e+02	382	5	5.0	256	14	Q9WM12	FUSION PROTEIN (FRAGME	9.24e+02
310	5	5.0	202	14	Q65842	COAT PROTEIN.	9.24e+02	383	5	5.0	259	5	Q18600	DVTRY-2 TRYPSIN PRECUS	9.24e+02
311	5	5.0	202	2	Q9WYA6	HYPOTHETICAL 22.9 KD P	9.24e+02	384	5	5.0	259	2	Q87819	OTSB PROTEIN.	9.24e+02
312	5	5.0	206	3	Q06346	CHROMOSOME IV COSMID 9	9.24e+02	385	5	5.0	259	5	Q23338	2C455.10 PROTEIN.	9.24e+02

386	5	5.0	260	5	015744	PKSB.	9.24e+02	459	5	5.0	363	5	023415	SIMILAR TO C. ELEGANS	9.24e+02
387	5	5.0	260	1	026344	SHIKIMATE 5-DEHYDROGEN	9.24e+02	460	5	5.0	364	10	Q04065	CATECHOL O-METHYLTRANS	9.24e+02
388	5	5.0	262	2	Q94DN0	CYSQ PROTEIN (CYSQ).	9.24e+02	461	5	5.0	365	5	Q97366	PRO-PHENOXIDASE ACTI	9.24e+02
389	5	5.0	262	13	Q90713	GALECTIN-3.	9.24e+02	462	5	5.0	366	14	Q90181	VIRAL ENV PROTEIN INTE	9.24e+02
390	5	5.0	263	1	058418	263AA LONG HYPOTHETICA	9.24e+02	463	5	5.0	366	2	Q41163	LIPOPROTEIN PRECURSOR.	9.24e+02
391	5	5.0	265	2	Q92CP3	UBIQUINONE/MENNAQUINONE	9.24e+02	464	5	5.0	367	2	Q9ZAP9	OUTER MEMBRANE LIPOPRO	9.24e+02
392	5	5.0	267	2	P70831	PERIPLASMIC SUBSTRATE-	9.24e+02	465	5	5.0	367	2	Q41164	LIPOPROTEIN PRECURSOR.	9.24e+02
393	5	5.0	269	5	Q24696	C-TYPE LECTIN-LIKE PRO	9.24e+02	466	5	5.0	369	5	Q19119	F02DB.3 PROTEIN.	9.24e+02
394	5	5.0	270	2	Q34852	PUTATIVE LYSINE-BINDIN	9.24e+02	467	5	5.0	370	14	Q81967	REGULATORY PROTEIN E2.	9.24e+02
395	5	5.0	271	5	Q9XVC6	C27C7.1 PROTEIN.	9.24e+02	468	5	5.0	370	2	Q9X517	NITROUS OXIDE REDUCTAS	9.24e+02
396	5	5.0	272	14	Q9WA93	MATRIX PROTEIN.	9.24e+02	469	5	5.0	371	5	Q9XZV6	G PROTEIN, BETA SUBUNI	9.24e+02
397	5	5.0	273	10	Q65150	OSMOTIC STRESS-INDUCED	9.24e+02	470	5	5.0	371	5	Q18110	T22H2.3 PROTEIN.	9.24e+02
398	5	5.0	273	10	Q82618	T9AA.8 PROTEIN.	9.24e+02	471	5	5.0	371	10	P93142	DIHIDROFLAVONOL REDUCT	9.24e+02
399	5	5.0	276	8	Q9XMU7	RIBOSOMAL PROTEIN S13.	9.24e+02	472	5	5.0	372	5	Q94254	SIMILAR TO TRANSPOSON	9.24e+02
400	5	5.0	277	2	Q927T1	CT504 HYPOTHETICAL PRO	9.24e+02	473	5	5.0	372	5	Q05247	HYPOTHETICAL 42.4 KD P	9.24e+02
401	5	5.0	280	2	Q48843	GENE CLUSTER.	9.24e+02	474	5	5.0	375	10	Q43023	ALCOHOL DEHYDROGENASE	9.24e+02
402	5	5.0	281	5	Q25344	L2759.5 PROTEIN.	9.24e+02	475	5	5.0	375	10	Q43027	ALCOHOL DEHYDROGENASE	9.24e+02
403	5	5.0	283	5	Q15923	DEOXYURIDINE TRIPOSPH	9.24e+02	476	5	5.0	375	2	Q9X514	NITROUS OXIDE REDUCTAS	9.24e+02
404	5	5.0	286	2	P77739	FROM BASES 1798041 TO	9.24e+02	477	5	5.0	375	2	Q9X513	NITROUS OXIDE REDUCTAS	9.24e+02
405	5	5.0	287	2	Q55924	HYPOTHETICAL 31.5 KD P	9.24e+02	478	5	5.0	375	2	Q9X512	NITROUS OXIDE REDUCTAS	9.24e+02
406	5	5.0	287	10	Q96307	SIMILAR TO DEHYDROGENA	9.24e+02	479	5	5.0	375	2	Q9X512	NITROUS OXIDE REDUCTAS	9.24e+02
407	5	5.0	288	2	Q07487	HYPOTHETICAL 31.7 KD P	9.24e+02	480	5	5.0	375	2	Q9X512	NITROUS OXIDE REDUCTAS	9.24e+02
408	5	5.0	291	10	Q92QT9	WERBP-1 PROTEIN.	9.24e+02	481	5	5.0	375	5	Q45815	ALCOHOL DEHYDROGENASE	9.24e+02
409	5	5.0	293	2	Q9X0U0	NADH DEHYDROGENASE, PU	9.24e+02	482	5	5.0	375	2	Q9X429	ACT-5 PROTEIN.	9.24e+02
410	5	5.0	295	13	Q93528	HOMEOBOX PROTEIN.	9.24e+02	483	5	5.0	375	2	Q9X502	NITROUS OXIDE REDUCTAS	9.24e+02
411	5	5.0	296	14	Q9YLN9	CAPSID PROTEIN VPI (FR	9.24e+02	484	5	5.0	375	2	Q9X502	NITROUS OXIDE REDUCTAS	9.24e+02
412	5	5.0	297	10	Q92PM4	PEPTIDE TRANSPORTER (F	9.24e+02	485	5	5.0	378	11	Q09010	ALCOHOL DEHYDROGENASE	9.24e+02
413	5	5.0	301	2	Q52907	PHOD PRECURSOR.	9.24e+02	486	5	5.0	379	10	Q65542	LUNATIC FRINGE PROTEIN	9.24e+02
414	5	5.0	301	6	P79136	F-ACTIN CAPPING PROTEI	9.24e+02	487	5	5.0	379	8	Q63854	HYPOTHETICAL 40.6 KD P	9.24e+02
415	5	5.0	303	14	Q65663	3A PROTEIN.	9.24e+02	488	5	5.0	380	14	Q74432	CYTCHROME B.	9.24e+02
416	5	5.0	303	10	Q80967	T16B24.22 PROTEIN.	9.24e+02	489	5	5.0	381	3	Q06815	SURFACE GLYCOPROTEIN (9.24e+02
417	5	5.0	310	2	Q9ZAI5	HYPOTHETICAL 34.6 KD P	9.24e+02	490	5	5.0	381	3	Q06815	CHROMOSOME XVI COSMID	9.24e+02
418	5	5.0	313	13	Q9THF0	AGRIN B19 ISOFORM (FRA	9.24e+02	491	5	5.0	381	5	Q18873	SIMILAR TO GUANINE NUC	9.24e+02
419	5	5.0	314	2	Q32102	YUUI PROTEIN.	9.24e+02	492	5	5.0	381	2	Q84910	GLYCOSYLTRANSFERASE WB	9.24e+02
420	5	5.0	315	5	Q26985	D1 PUTATIVE CYSTEINE P	9.24e+02	493	5	5.0	381	14	Q87392	ENVELOPE GLYCOPROTEIN	9.24e+02
421	5	5.0	317	5	Q23349	COSMID ZC487.	9.24e+02	494	5	5.0	383	14	Q9YP16	ENVELOPE GLYCOPROTEIN	9.24e+02
422	5	5.0	318	2	Q92398	CITRATE SYNTHASE (EC 4	9.24e+02	495	5	5.0	385	14	Q87296	HYPOTHETICAL 43.8 KD P	9.24e+02
423	5	5.0	319	4	Q92596	FICOLIN.	9.24e+02	496	5	5.0	385	14	Q87309	ENVELOPE GLYCOPROTEIN	9.24e+02
424	5	5.0	319	5	Q02637	CARBONIC ANHYDRASE (EC	9.24e+02	497	5	5.0	386	14	Q87437	ENVELOPE GLYCOPROTEIN	9.24e+02
425	5	5.0	319	5	Q83552	GTP-BINDING PROTEIN (E	9.24e+02	498	5	5.0	387	2	Q86737	PUTATIVE ADENOSINE DEA	9.24e+02
426	5	5.0	319	13	Q93529	FORKEAD-DOMAIN-CONTAI	9.24e+02	499	5	5.0	388	5	Q01324	F18A11.2 PROTEIN.	9.24e+02
427	5	5.0	319	2	Q54221	PUTATIVE CYCLASE/DEHYD	9.24e+02	500	5	5.0	388	5	Q44609	R09B5.12 PROTEIN.	9.24e+02
428	5	5.0	319	2	Q9XW16	PUTATIVE PORPHOBILINO	9.24e+02	501	5	5.0	388	14	Q29592	POLYPROTEIN (FRAGMENT)	9.24e+02
429	5	5.0	322	2	Q92336	CITRATE SYNTHASE (EC 4	9.24e+02	502	5	5.0	389	3	Q14001	HYPOTHETICAL 45.1 KD P	9.24e+02
430	5	5.0	324	14	Q89914	SC4.	9.24e+02	503	5	5.0	389	10	Q24395	SERINE-THREONINE PROTE	9.24e+02
431	5	5.0	324	5	Q18412	COSMID C33H5.	9.24e+02	504	5	5.0	390	14	Q87440	ENVELOPE GLYCOPROTEIN	9.24e+02
432	5	5.0	327	5	Q22984	HELIX-TURN-HELIX DNA B	9.24e+02	505	5	5.0	391	14	Q87398	ENVELOPE GLYCOPROTEIN	9.24e+02
433	5	5.0	330	2	Q34308	COMPLEMENT FACTOR H-RE	9.24e+02	506	5	5.0	392	10	Q56487	ABSCISSION POLYGALACTU	9.24e+02
434	5	5.0	331	4	Q92496	HYPOHETICAL 36.1 KD P	9.24e+02	507	5	5.0	393	14	Q87430	ENVELOPE GLYCOPROTEIN	9.24e+02
435	5	5.0	333	2	Q9XAB9	HYPOHETICAL 36.1 KD P	9.24e+02	508	5	5.0	397	1	Q93777	F12A24.8 PROTEIN.	9.24e+02
436	5	5.0	334	5	Q9XVP9	F30A10.5 PROTEIN.	9.24e+02	509	5	5.0	397	4	Q15735	397AA LONG HYPOTHETICA	9.24e+02
437	5	5.0	335	11	Q07646	PEGL/MEST PROTEIN.	9.24e+02	510	5	5.0	397	4	Q15735	PHOSPHATIDYLINOSITOL (9.24e+02
438	5	5.0	336	2	Q25731	GLUCOKINASE (GLK).	9.24e+02	511	5	5.0	398	2	Q24939	HYPOTHETICAL 45.3 KD P	9.24e+02
439	5	5.0	336	13	Q98977	COMPLEMENT COMPONENT C	9.24e+02	512	5	5.0	399	2	Q9A9W9	PUTATIVE TRANSPORT ASS	9.24e+02
440	5	5.0	337	9	Q38085	HYPOHETICAL 39.9 KD P	9.24e+02	513	5	5.0	399	5	Q96770	GLUTAMINE SYNTHETASE (9.24e+02
441	5	5.0	337	2	Q9ADN2	PDUO.	9.24e+02	514	5	5.0	399	11	Q35137	ARISTALESS HOMEOBOX-4	9.24e+02
442	5	5.0	340	5	P91500	F40G12.6 PROTEIN.	9.24e+02	515	5	5.0	400	14	Q9WJ09	HYPOTHETICAL 44.7 KD P	9.24e+02
443	5	5.0	343	5	Q20245	COSMID T28A11.	9.24e+02	516	5	5.0	402	4	Q9Y6VA	KIF3 (FRAGMENT)	9.24e+02
444	5	5.0	344	5	P91507	HYPOHETICAL 37.8 KD P	9.24e+02	517	5	5.0	403	2	Q9WZ11	CRATINASE (EC 3.5.3.3	9.24e+02
445	5	5.0	344	8	Q83729	NADH DEHYDROGENASE SUB	9.24e+02	518	5	5.0	403	2	Q45380	DNA FOR LIPOPOLYSACCHA	9.24e+02
446	5	5.0	346	8	Q21215	NADH DEHYDROGENASE SUB	9.24e+02	519	5	5.0	406	14	Q9WF43	HEMAGGLUTININ (FRAGEN	9.24e+02
447	5	5.0	346	8	Q21144	NADH DEHYDROGENASE SUB	9.24e+02	520	5	5.0	406	14	Q9WF43	HEMAGGLUTININ (FRAGEN	9.24e+02
448	5	5.0	346	8	Q21195	NADH DEHYDROGENASE SUB	9.24e+02	521	5	5.0	408	2	Q83830	HYPOHETICAL 43.4 KD P	9.24e+02
449	5	5.0	347	8	Q21211	NADH DEHYDROGENASE SUB	9.24e+02	522	5	5.0	409	5	Q24080	DSHC.	9.24e+02
450	5	5.0	347	8	Q21211	NADH DEHYDROGENASE SUB	9.24e+02	523	5	5.0	409	5	Q19414	F13E9.4 PROTEIN.	9.24e+02
451	5	5.0	348	8	Q21305	NADH DEHYDROGENASE SUB	9.24e+02	524	5	5.0	412	14	Q53354	ORF C (FRAGMENT).	9.24e+02
452	5	5.0	348	8	Q92253	NADH DEHYDROGENASE SUB	9.24e+02	525	5	5.0	412	14	P74200	PENICILLIN-BINDING PRO	9.24e+02
453	5	5.0	349	2	Q06007	NADP-DEPENDENT ALCOHOL	9.24e+02	526	5	5.0	415	6	Q28177	PHAKIN.	9.24e+02
454	5	5.0	351	5	Q45372	F15H9.2 PROTEIN.	9.24e+02	527	5	5.0	415	11	Q920K4	INTERLEUKIN-5 RECEPTOR	9.24e+02
455	5	5.0	355	4	Q9Y5W3	KRUPPEL-LIKE ZINC FING	9.24e+02	528	5	5.0	416	14	Q9YR86	VIRAL RNA-DEPENDENT RN	9.24e+02
456	5	5.0	360	10	P87046	OXYSTEROL-BINDING PROT	9.24e+02	529	5	5.0	416	5	Q16353	F13H6.5 PROTEIN.	9.24e+02
457	5	5.0	360	10	Q82391	T27A16.26 PROTEIN.	9.24e+02	530	5	5.0	417	4	Q43820	SIMILAR TO HYALURONOGL	9.24e+02
458	5	5.0	361	1	Q59364	361AA LONG HYPOTHETICA	9.24e+02	531	5	5.0	418	5	Q17239	K10B4.4 PROTEIN.	9.24e+02
											418	2	Q9X2H0	SUGAR ABC TRANSPORTER,	9.24e+02

532	5	5.0	419 14	P87662	TRANSCRIPTIONAL PROTEI	9.24e+02	605	5	5.0	505 5	001328	F4GA8.2 PROTEIN.	9.24e+02
533	5	5.0	419 2	O68526	SYMBIOSIS ISLAND INTEG	9.24e+02	606	5	5.0	506 5	Q23576	SIMILAR TO SODIUM/PHOP	9.24e+02
534	5	5.0	420 14	O9YPD5	MBV AUSTRALIAN ISOLATE	9.24e+02	607	5	5.0	507 11	O26720	ZNT-1.	9.24e+02
535	5	5.0	420 11	O9WV60	GLYCOCEN SYNTHASE KINA	9.24e+02	608	5	5.0	510 5	O44382	SLIMB.	9.24e+02
536	5	5.0	420 15	O39624	COSMID F20B4.	9.24e+02	609	5	5.0	510 3	O93992	HYPOTHETICAL MEMBRANE	9.24e+02
537	5	5.0	421 13	O39H60	GLYCOCEN SYNTHASE KINA	9.24e+02	610	5	5.0	511 14	O89664	(STRAIN 87-VC-B).	9.24e+02
538	5	5.0	421 10	O39048	CER2 GENE.	9.24e+02	611	5	5.0	511 14	O89000	(STRAIN 86-DF-P) GLYCO	9.24e+02
539	5	5.0	422 4	O9Y353	SOLUBLE LIVER ANTIGEN/	9.24e+02	612	5	5.0	511 14	O89625	(STRAIN 83-HD-B1).	9.24e+02
540	5	5.0	424 10	O41109	REGULATOR OF MAT2.	9.24e+02	613	5	5.0	511 14	O88996	(STRAIN 84-PN-H) GLYCO	9.24e+02
541	5	5.0	426 2	O67578	FLAGELLAR HOOK ASSOCIA	9.24e+02	614	5	5.0	511 14	O89007	(STRAIN 84-PN-B2) GLYC	9.24e+02
542	5	5.0	428 2	O32975	ATPASE.	9.24e+02	615	5	5.0	511 14	O89008	(STRAIN 85-ES-B2) GLYC	9.24e+02
543	5	5.0	431 2	O45081	MOPA.	9.24e+02	616	5	5.0	513 2	O48246	VACUOLATING CITOTOXIN	9.24e+02
544	5	5.0	435 4	O13309	CYCLIN A/CDK2-ASSOCIAT	9.24e+02	617	5	5.0	513 2	O9WZ23	2-ISOPROPYLMALATE SYNT	9.24e+02
545	5	5.0	437 5	O18379	DOPA DECARBOXYLASE (DD	9.24e+02	618	5	5.0	513 14	O88094	GLYCOPROTEIN 120.	9.24e+02
546	5	5.0	437 2	O57387	HASA, HASD AND HASE GE	9.24e+02	619	5	5.0	516 14	O87970	GLYCOPROTEIN 120.	9.24e+02
547	5	5.0	439 1	O93689	HYPOTHETICAL 50.9 KD P	9.24e+02	620	5	5.0	516 10	O65513	HYPOTHETICAL 56.3 KD P	9.24e+02
548	5	5.0	441 2	O07386	HISTIDINE KINASE.	9.24e+02	621	5	5.0	517 5	O96509	AXONEMAL DYNEIN INTERM	9.24e+02
549	5	5.0	443 2	O34417	METALLOPROTEINASE TRANSP	9.24e+02	622	5	5.0	518 2	O34512	YPMW PROTEIN.	9.24e+02
550	5	5.0	445 10	O41337	FEEBLY.	9.24e+02	623	5	5.0	518 3	O59896	LACCASE PRECURSOR (EC	9.24e+02
551	5	5.0	446 6	O19071	ALPHA-1,6-MANNOSYL-GLY	9.24e+02	624	5	5.0	519 2	O9X991	FRUB.	9.24e+02
552	5	5.0	448 11	O9WVH8	DEVELOPMENTAL ARTERIES	9.24e+02	625	5	5.0	520 5	O45317	Y17D7A.4 PROTEIN.	9.24e+02
553	5	5.0	448 14	O83457	FIBRE.	9.24e+02	626	5	5.0	521 14	O87462	ENVELOPE GLYCOPROTEIN	9.24e+02
554	5	5.0	448 2	O92N87	BETA-GLUCOSIDASE.	9.24e+02	627	5	5.0	521 14	O87463	ENVELOPE GLYCOPROTEIN	9.24e+02
555	5	5.0	450 13	O39809	INTERMEDIATE FILAMENT	9.24e+02	628	5	5.0	522 2	O55984	HYPOTHETICAL 58.4 KD P	9.24e+02
556	5	5.0	452 1	O29870	ACETYL-COA DECARBOXYLA	9.24e+02	629	5	5.0	522 14	O87465	ENVELOPE GLYCOPROTEIN	9.24e+02
557	5	5.0	452 14	O07045	D6L PROTEIN.	9.24e+02	630	5	5.0	522 14	O87461	ENVELOPE GLYCOPROTEIN	9.24e+02
558	5	5.0	454 4	O9Y2T3	GUANINE DEAMINASE GDA.	9.24e+02	631	5	5.0	523 10	O92V69	PUTATIVE UBIQUITIN ACT	9.24e+02
559	5	5.0	455 8	O47056	RIBULOSE BISPHOSPHATE	9.24e+02	632	5	5.0	524 14	O87454	ENVELOPE GLYCOPROTEIN	9.24e+02
560	5	5.0	455 10	O92VAL	F9K20.13 PROTEIN.	9.24e+02	633	5	5.0	525 14	O87460	ENVELOPE GLYCOPROTEIN	9.24e+02
561	5	5.0	455 2	O92A79	ENTD.	9.24e+02	634	5	5.0	525 14	O87466	ENVELOPE GLYCOPROTEIN	9.24e+02
562	5	5.0	460 5	O22106	SIMILAR TO ACETLY-COA	9.24e+02	635	5	5.0	525 14	O87455	ENVELOPE GLYCOPROTEIN	9.24e+02
563	5	5.0	462 2	O52801	PCZA361.14.	9.24e+02	636	5	5.0	526 4	O75567	RAF RESPONSIVE ZINC FI	9.24e+02
564	5	5.0	463 4	O60540	HYALURONIDASE.	9.24e+02	637	5	5.0	527 14	O87458	ENVELOPE GLYCOPROTEIN	9.24e+02
565	5	5.0	465 2	O51601	2-HALOENZOATE 1,2-DIO	9.24e+02	638	5	5.0	527 14	O87468	ENVELOPE GLYCOPROTEIN	9.24e+02
566	5	5.0	467 5	O16315	COS8.7 PROTEIN.	9.24e+02	639	5	5.0	530 10	O04892	CYTOCHROME P450 LIKE.T	9.24e+02
567	5	5.0	467 8	O33404	RIBULOSE BISPHOSPHATE	9.24e+02	640	5	5.0	531 4	Q15043	KIAA0062 PROTEIN (FRAG	9.24e+02
568	5	5.0	469 5	O20752	F54C9.2 PROTEIN.	9.24e+02	641	5	5.0	531 3	O74858	LYSLY-TRNA SYNTHETASE.	9.24e+02
569	5	5.0	469 8	P94057	RIBULOSE BISPHOSPHATE	9.24e+02	642	5	5.0	531 10	O82416	TYROSINE/DOPA DECARBOX	9.24e+02
570	5	5.0	470 14	O9WSX5	UL38 PROTEIN.	9.24e+02	643	5	5.0	531 10	O43014	BETA-GLUCOSIDASE (EC 3	9.24e+02
571	5	5.0	471 2	O83871	CONSERVED HYPOTHETICAL	9.24e+02	644	5	5.0	532 10	O81849	HYPOTHETICAL 60.3 KD P	9.24e+02
572	5	5.0	471 10	O9XIB2	F13P21.11 PROTEIN.	9.24e+02	645	5	5.0	535 2	O56676	MANNOSE-SENSITIVE HEMA	9.24e+02
573	5	5.0	472 5	O95656	HYPOTHETICAL 52.6 KD P	9.24e+02	646	5	5.0	535 2	O59141	CHITINASE PRECURSOR (E	9.24e+02
574	5	5.0	473 5	O20924	F57B1.2 PROTEIN.	9.24e+02	647	5	5.0	542 2	O86368	FADE8.	9.24e+02
575	5	5.0	474 11	O9WUM4	CORONIN-3.	9.24e+02	648	5	5.0	543 5	O20720	F53F4.11 PROTEIN.	9.24e+02
576	5	5.0	476 8	O32088	RIBULOSE BISPHOSPHATE	9.24e+02	649	5	5.0	543 5	O14879	MUCIN (FRAGMENT).	9.24e+02
577	5	5.0	478 2	O86666	PUTATIVE SUGAR TRANSFE	9.24e+02	650	5	5.0	543 5	O45069	CL11D2.4 PROTEIN.	9.24e+02
578	5	5.0	481 14	O9WRJ0	ENVELOPE GLYCOPROTEIN	9.24e+02	651	5	5.0	544 10	O22915	G-BETA-REPEAT CONTAINI	9.24e+02
579	5	5.0	483 1	O58952	483AA LONG HYPOTHETICA	9.24e+02	652	5	5.0	545 5	O27621	CARBOXYLESTERASE (EC 3	9.24e+02
580	5	5.0	483 10	O40490	CYCLIN A-LIKE PROTEIN.	9.24e+02	653	5	5.0	548 5	O16177	ESTERASE 5A PRECURSOR	9.24e+02
581	5	5.0	483 5	O22698	SIMILAR TO GLYCOSYLTRA	9.24e+02	654	5	5.0	550 4	O43405	COCH-5B2.	9.24e+02
582	5	5.0	485 11	O35667	MAX DIMERIZATION PROTE	9.24e+02	655	5	5.0	553 14	O9WF46	FUSION GLYCOPROTEIN PR	9.24e+02
583	5	5.0	485 2	O9X390	PX01-133.	9.24e+02	656	5	5.0	553 14	O9WI28	F PROTEIN.	9.24e+02
584	5	5.0	486 2	O84116	HYPOTHETICAL 55.2 KD P	9.24e+02	657	5	5.0	553 2	O9ZJ35	PUTATIVE.	9.24e+02
585	5	5.0	486 10	O04591	SEQUENCE OF BAC F19K23	9.24e+02	658	5	5.0	553 14	O83847	FUSION GLYCOPROTEIN PR	9.24e+02
586	5	5.0	486 10	O22909	HYPOTHETICAL PROTEIN.	9.24e+02	659	5	5.0	554 5	O45089	ZK994.1 PROTEIN.	9.24e+02
587	5	5.0	486 2	P72269	HOMOLOGUE OF HYPOTHEI	9.24e+02	660	5	5.0	559 2	O83432	APOLIPOPROTEIN N-ACYLT	9.24e+02
588	5	5.0	487 2	O47553	ORF8.	9.24e+02	661	5	5.0	560 14	O9WQW9	HEMAGGLUTININ (FRAGMEN	9.24e+02
589	5	5.0	489 14	O9WBL2	NUCLEOCAPSID PROTEIN.	9.24e+02	662	5	5.0	560 11	O62634	BRAIN SPECIFIC NA+-DEP	9.24e+02
590	5	5.0	489 14	O9WJ25	ORF OP-1.	9.24e+02	663	5	5.0	561 5	O76134	NRK-RELATED KINASE.	9.24e+02
591	5	5.0	489 14	O9WMM9	NUCLEOCAPSID PROTEIN.	9.24e+02	664	5	5.0	562 14	O67140	HEMAGGLUTININ.	9.24e+02
592	5	5.0	489 14	O34980	PROLINE PERMEASE (FRAG	9.24e+02	665	5	5.0	562 14	O67143	HEMAGGLUTININ.	9.24e+02
593	5	5.0	489 2	O54980	SURFACE ENVELOPE GLYCO	9.24e+02	666	5	5.0	562 14	O67144	HEMAGGLUTININ.	9.24e+02
594	5	5.0	489 14	O88107	SURFACE ENVELOPE GLYCO	9.24e+02	667	5	5.0	562 14	O67016	HEMAGGLUTININ.	9.24e+02
595	5	5.0	489 2	O47553	PROLINE PERMEASE (FRAG	9.24e+02	668	5	5.0	562 14	O67011	HEMAGGLUTININ.	9.24e+02
596	5	5.0	490 2	O9W779	UDP-N-ACETYLMURAMOYLAL	9.24e+02	669	5	5.0	562 14	O67326	HEMAGGLUTININ.	9.24e+02
597	5	5.0	490 5	O45920	Y37A1A.3 PROTEIN.	9.24e+02	670	5	5.0	562 14	O67327	HEMAGGLUTININ.	9.24e+02
598	5	5.0	490 14	O88120	SURFACE ENVELOPE GLYCO	9.24e+02	671	5	5.0	562 14	O67120	HEMAGGLUTININ.	9.24e+02
599	5	5.0	491 2	O51279	HEAT SHOCK PROTEIN 70	9.24e+02	672	5	5.0	562 14	O67123	HEMAGGLUTININ.	9.24e+02
600	5	5.0	494 13	O73621	UTROPHIN (DYSTROPHIN-R	9.24e+02	673	5	5.0	564 14	O72736	A54R PROTEIN.	9.24e+02
601	5	5.0	495 10	O92UX1	PUTATIVE CYTOCHROME P4	9.24e+02	674	5	5.0	565 14	O88254	F PROTEIN.	9.24e+02
602	5	5.0	495 10	O22217	T3266.7 PROTEIN.	9.24e+02	675	5	5.0	565 14	O88259	F PROTEIN.	9.24e+02
603	5	5.0	497 2	O51503	HYPOTHETICAL 59.3 KD P	9.24e+02	676	5	5.0	566 14	O9WCE6	HEMAGGLUTININ PRECURSO	9.24e+02
604	5	5.0	503 14	O9W544	U10 PROTEIN.	9.24e+02	677	5	5.0	566 14	O9WCE4	HEMAGGLUTININ PRECURSO	9.24e+02

678	5	5.0	566 14	Q9WCE8	HEMAGGLUTININ PRECURSO	9.24e+02	751	5	5.0	642	3	Q9X7T0	HYPOHETICAL DNAJ DOMA	9.24e+02
679	5	5.0	566 14	Q9WCE3	HEMAGGLUTININ PRECURSO	9.24e+02	752	5	5.0	642	5	P76016	DHAR PROTEIN.	9.24e+02
680	5	5.0	566 14	Q9WCE2	HEMAGGLUTININ PRECURSO	9.24e+02	753	5	5.0	645	5	Q09478	PUTATIVE 70.0 KD ZINC	9.24e+02
681	5	5.0	566 14	Q9WCE5	HEMAGGLUTININ PRECURSO	9.24e+02	754	5	5.0	650	5	Q02306	T09E11.4 PROTEIN.	9.24e+02
682	5	5.0	566 14	Q9WCD9	HEMAGGLUTININ PRECURSO	9.24e+02	755	5	5.0	655	5	Q04832	HYDROGENOSOMAL CHAPERON	9.24e+02
683	5	5.0	566 14	Q9WCD8	HEMAGGLUTININ PRECURSO	9.24e+02	756	5	5.0	660	2	O25815	CONSERVED HYPOTHETICAL	9.24e+02
684	5	5.0	566 14	Q9WCE1	HEMAGGLUTININ PRECURSO	9.24e+02	757	5	5.0	660	14	O41172	ENV.	9.24e+02
685	5	5.0	566 14	Q9WCE0	HEMAGGLUTININ PRECURSO	9.24e+02	758	5	5.0	661	10	O22577	ARM REPEAT CONTAINING	9.24e+02
686	5	5.0	566 14	Q9WCE7	HEMAGGLUTININ PRECURSO	9.24e+02	759	5	5.0	662	5	P91331	COSMID F54H5.	9.24e+02
687	5	5.0	566 14	Q9WCE2	HEMAGGLUTININ.	9.24e+02	760	5	5.0	662	5	Q09512	HYPOTHETICAL 76.7 KD P	9.24e+02
688	5	5.0	566 11	Q62977	MITOGEN-ACTIVATED ZINC	9.24e+02	761	5	5.0	664	10	O49319	PUTATIVE POLYGALACTURO	9.24e+02
689	5	5.0	566 12	Q32309	NEUTRAL PROTEASE A.	9.24e+02	762	5	5.0	669	2	Q56151	P-AMINOBENZOIC ACID SY	9.24e+02
690	5	5.0	566 14	Q89459	HEMAGGLUTININ.	9.24e+02	763	5	5.0	673	4	Q04859	KIAA0759 PROTEIN (FRAG	9.24e+02
691	5	5.0	566 14	O84114	HEMAGGLUTININ.	9.24e+02	764	5	5.0	675	2	O87906	INSECTICIDAL PROTEIN J	9.24e+02
692	5	5.0	566 14	O82770	HEMAGGLUTININ.	9.24e+02	765	5	5.0	683	14	O11780	TRANSFORMING GROWTH FA	9.24e+02
693	5	5.0	566 14	Q98095	HEMAGGLUTININ.	9.24e+02	766	5	5.0	683	10	Q92046	PUTATIVE COPIA-LIKE RE	9.24e+02
694	5	5.0	566 14	Q98094	HEMAGGLUTININ.	9.24e+02	767	5	5.0	690	5	Q9XUC6	M162.7 PROTEIN.	9.24e+02
695	5	5.0	566 14	Q98092	HEMAGGLUTININ.	9.24e+02	768	5	5.0	690	3	Q74874	PUTATIVE TRANSCRIPTION	9.24e+02
696	5	5.0	566 4	O60273	KIAA0520 PROTEIN (FRAG	9.24e+02	769	5	5.0	693	5	O61920	C18G1.4 PROTEIN.	9.24e+02
697	5	5.0	569 4	Q91213	BETA-TRANSDUCIN REPEAT	9.24e+02	770	5	5.0	694	14	Q9YNA9	ENV PROTEIN.	9.24e+02
698	5	5.0	570 3	Q06150	CHROMOSOME XII COSMID	9.24e+02	771	5	5.0	694	14	Q9YNA5	ENV PROTEIN.	9.24e+02
699	5	5.0	571 14	Q9YX79	HN HEMAGGLUTININ-NURAM	9.24e+02	772	5	5.0	696	5	O17034	IMMUNE FACTOR.	9.24e+02
700	5	5.0	571 14	Q9YX78	HN HEMAGGLUTININ-NURAM	9.24e+02	773	5	5.0	697	3	O74504	HYPOTHETICAL 77.8 KD P	9.24e+02
701	5	5.0	571 14	Q9W919	HEMAGGLUTININ-NEURAMIN	9.24e+02	774	5	5.0	698	8	O98651	NADH DEHYDROGENASE SUB	9.24e+02
702	5	5.0	571 14	Q9W9B1	HEMAGGLUTININ-NEURAMIN	9.24e+02	775	5	5.0	698	8	O98642	ENV MRNA.	9.24e+02
703	5	5.0	571 14	Q9W9C1	HEMAGGLUTININ-NEURAMIN	9.24e+02	776	5	5.0	699	14	Q69384	POLYRIBONUCLEOTIDE NUC	9.24e+02
704	5	5.0	571 14	Q9W9C2	HEMAGGLUTININ-NEURAMIN	9.24e+02	777	5	5.0	701	2	O87792	POLYPHOSPHATE KINASE.	9.24e+02
705	5	5.0	571 14	Q9W129	HN PROTEIN.	9.24e+02	778	5	5.0	701	2	O86073	KINESIN FAMILY MEMBER	9.24e+02
706	5	5.0	571 14	Q83851	HEMAGGLUTININ-NEURAMIN	9.24e+02	779	5	5.0	702	2	O86988	UMOB.	9.24e+02
707	5	5.0	574 14	Q9YS24	FUSION GLYCOPROTEIN PR	9.24e+02	780	5	5.0	702	2	O86988	1-DEOXY-D-XYLULOSE 5-P	9.24e+02
708	5	5.0	574 14	O89535	FUSION PROTEIN.	9.24e+02	781	5	5.0	710	5	Q96694	HYPOTHETICAL 80.9 KD P	9.24e+02
709	5	5.0	576 14	O80459	PUTATIVE NICOTINATE PH	9.24e+02	782	5	5.0	711	2	Q9WYS9	TRIP PROTEIN (FRAGMENT	9.24e+02
710	5	5.0	576 14	O41623	ENVELOPE GLYCOPROTEIN	9.24e+02	783	5	5.0	711	11	O88679	FIBULIN-1 ISOFORM C PR	9.24e+02
711	5	5.0	576 14	Q86677	HEMAGGLUTININ (FRAGMEN	9.24e+02	784	5	5.0	712	5	O77469	CHROMOSOME XV READING	9.24e+02
712	5	5.0	577 14	Q9WCW3	HEMAGGLUTININ-NEURAMIN	9.24e+02	785	5	5.0	720	2	Q92876	GLUCAN BRANCHING ENZYM	9.24e+02
713	5	5.0	577 14	Q9W9H0	HEMAGGLUTININ-NEURAMIN	9.24e+02	786	5	5.0	725	10	Q39659	TETRAFUNCTIONAL PROTEIN	9.24e+02
714	5	5.0	577 14	O90340	HEMAGGLUTININ-NEURAMIN	9.24e+02	787	5	5.0	735	1	O36457	CONSERVED PROTEIN.	9.24e+02
715	5	5.0	577 14	Q9W828	HEMAGGLUTININ-NEURAMIN	9.24e+02	788	5	5.0	745	1	Q9Y9L3	745AA LONG HYPOTHETICA	9.24e+02
716	5	5.0	577 14	O76408	TI0B5.5 PROTEIN.	9.24e+02	789	5	5.0	748	14	O9YR01	COS54.1 PRECURSOR (FRA	9.24e+02
717	5	5.0	581 14	Q93850	HAEMAGGLUTININ-NEURAMI	9.24e+02	790	5	5.0	748	2	O35260	CAG PATHOGENICITY ISLA	9.24e+02
718	5	5.0	583 3	Q12372	CHROMOSOME XII READING	9.24e+02	791	5	5.0	749	14	Q9WU06	ENVELOPE GLYCOPROTEIN	9.24e+02
719	5	5.0	586 2	Q9WX29	PUTATIVE ARGINYL-TRNA	9.24e+02	792	5	5.0	749	5	Q02602	HYPOTHETICAL PROTEIN I	9.24e+02
720	5	5.0	587 2	O25510	OUTER MEMBRANE PROTEIN	9.24e+02	793	5	5.0	758	4	Q16891	MOTOR PROTEIN.	9.24e+02
721	5	5.0	589 3	Q08295	CHROMOSOME XV READING	9.24e+02	794	5	5.0	759	3	O14267	HYPOTHETICAL 83.4 KD P	9.24e+02
722	5	5.0	589 2	P96439	EXPDI.	9.24e+02	795	5	5.0	762	5	O27701	INS-1 WINGED HELIX.	9.24e+02
723	5	5.0	590 2	Q9ZM78	PUTATIVE.	9.24e+02	796	5	5.0	771	11	P97691	HYPOTHETICAL 83.8 KD P	9.24e+02
724	5	5.0	592 11	Q9W7X8	SODIUM-COUPLED ASCORBI	9.24e+02	797	5	5.0	774	2	O32880	CODED FOR BY C. ELEGAN	9.24e+02
725	5	5.0	593 13	Q9W677	LIM DOMAIN INTERACTING	9.24e+02	798	5	5.0	774	5	O23424	REGULATORY PROTEIN VIV	9.24e+02
726	5	5.0	594 11	O88402	SYNAPTOJANIN 2 ISOFORM	9.24e+02	799	5	5.0	780	10	O04346	SP4 TRANSCRIPTION FACT	9.24e+02
727	5	5.0	595 2	O55725	2-SUCCINYL-6-HYDROXY-2	9.24e+02	800	5	5.0	784	4	O60402	COXI INTRON2 ORF.	9.24e+02
728	5	5.0	599 3	Q10988	UV-ENDORNUCLEASE.	9.24e+02	801	5	5.0	802	8	O35062	BROMODOMAIN PROTEIN.	9.24e+02
729	5	5.0	601 5	O77459	KEN PROTEIN.	9.24e+02	802	5	5.0	803	3	O74964	KIAA0792 PROTEIN.	9.24e+02
730	5	5.0	606 2	O66380	SPAA.	9.24e+02	803	5	5.0	807	4	O94886	COSMID C18F10.	9.24e+02
731	5	5.0	609 4	Q12886	CALCIUM-ACTIVATED POTA	9.24e+02	804	5	5.0	808	5	Q18098	RAB8 INTERACTING PROTE	9.24e+02
732	5	5.0	610 2	O51577	EXODEOXYRIBONUCLEASE V	9.24e+02	805	5	5.0	821	11	Q61161	CELLULOSE DEHYDROGENA	9.24e+02
733	5	5.0	614 5	O46149	WEEL-LIKE KINASE.	9.24e+02	806	5	5.0	822	2	Q9ZHG7	HYPOHETICAL 92.4 KD P	9.24e+02
734	5	5.0	615 14	Q93758	HEMAGGLUTININ-NEURAMIN	9.24e+02	807	5	5.0	828	3	O74240	CELLOBIOSYL DEHYDROGENA	9.24e+02
735	5	5.0	616 14	Q93852	HEMAGGLUTININ-NEURAMIN	9.24e+02	808	5	5.0	828	2	O68107	HYPOHETICAL 86.4 KD P	9.24e+02
736	5	5.0	616 14	Q84837	ORE 3 (FRAGMENT).	9.24e+02	809	5	5.0	830	4	Q14162	KIAA0149 PROTEIN.	9.24e+02
737	5	5.0	617 5	Q9XWZ2	F45F3A.3 PROTEIN.	9.24e+02	810	5	5.0	832	14	Q9YPU5	DNA POLYMERASE.	9.24e+02
738	5	5.0	618 5	Q18693	F28F8-2 PROTEIN.	9.24e+02	811	5	5.0	834	11	O88941	GLYCOPROTEIN PROCESSIN	9.24e+02
739	5	5.0	619 4	O75358	NEUROAN1.	9.24e+02	812	5	5.0	835	2	O25908	PUTATIVE ADENINE SPECI	9.24e+02
740	5	5.0	620 5	O16519	T05H4.14 PROTEIN.	9.24e+02	813	5	5.0	837	4	O3Y488	HYPOHETICAL 91.8 KD P	9.24e+02
741	5	5.0	620 10	O81008	PUTATIVE AMINO-ACID AC	9.24e+02	814	5	5.0	838	9	O64330	GP16.	9.24e+02
742	5	5.0	623 5	Q27560	SERINE/THREONINE PROTE	9.24e+02	815	5	5.0	842	10	O49527	POLLEN-SPECIFIC PROTEI	9.24e+02
743	5	5.0	624 5	O61393	GLY5C (EC 2.4.1.41) (P	9.24e+02	816	5	5.0	843	14	Q03766	DNA POLYMERASE IEC 2.7	9.24e+02
744	5	5.0	626 5	O61392	GLY5B (EC 2.4.1.41) (P	9.24e+02	817	5	5.0	845	10	O49289	SIMILAR ATP-DEPENDENT	9.24e+02
745	5	5.0	629 10	Q39174	PUTATIVE ALCOHOL DEHYD	9.24e+02	818	5	5.0	845	3	O94719	HYPOHETICAL 94.5 KD P	9.24e+02
746	5	5.0	633 11	P70419	UDP-GALNAC:POLYPEPTIDE	9.24e+02	819	5	5.0	853	1	O30772	AMYLLOPULLULANASE.	9.24e+02
747	5	5.0	633 14	Q65863	FUSION PROTEIN (FRAGME	9.24e+02	820	5	5.0	858	14	O74114	GP160.	9.24e+02
748	5	5.0	634 5	Q17474	B0334.3A PROTEIN.	9.24e+02	821	5	5.0	862	14	Q9WQ12	ENV POLYPROTEIN.	9.24e+02
749	5	5.0	639 13	Q01707	CONVERTASE PC2.	9.24e+02	822	5	5.0	862	14	Q9WLD7	ENVELOPE GLYCOPROTEIN.	9.24e+02
750	5	5.0	640 14	Q9WAT4	MINOR CORE PROTEIN VP4	9.24e+02	823	5	5.0					
			641 5	Q9Y026	BCDNA.LD22679.	9.24e+02								

824	5	5.0	865	14	Q9WIU7	ENVELOPE GLYCOPROTEIN	9.24e+02	897	5	5.0	1102	2	P95684	SUBTILISIN-LIKE PROTEA	9.24e+02
825	5	5.0	865	14	Q9WIU3	ENVELOPE GLYCOPROTEIN	9.24e+02	898	5	5.0	1110	13	Q91255	NF-180.	9.24e+02
826	5	5.0	865	14	Q9WIU3	ENVELOPE GLYCOPROTEIN	9.24e+02	899	5	5.0	1115	14	Q83484	130 KD PROTEIN.	9.24e+02
827	5	5.0	865	14	Q9WIU4	ENVELOPE GLYCOPROTEIN	9.24e+02	900	5	5.0	1119	5	O77374	PFC0810C PROTEIN.	9.24e+02
828	5	5.0	865	14	Q9WIU8	ENVELOPE GLYCOPROTEIN	9.24e+02	901	5	5.0	1123	14	O66933	POLYMERASE (FRAGMENT).	9.24e+02
829	5	5.0	867	2	Q9XBS2	MEMBRANE ALANYL AMINOP	9.24e+02	902	5	5.0	1128	11	O88442	AORTIC CARBOXYPEPTIDAS	9.24e+02
830	5	5.0	871	5	O76976	SUDF98 PROTEIN.	9.24e+02	903	5	5.0	1132	14	Q07022	M POLYPROTEIN PRECURSO	9.24e+02
831	5	5.0	873	4	Q9V652	VITAMIN D RECEPTOR-INT	9.24e+02	904	5	5.0	1137	13	Q9W6F6	M POLYPROTEIN TYROSINE KINA	9.24e+02
832	5	5.0	877	14	O55596	PUTATIVE DNA-DIRECTED	9.24e+02	905	5	5.0	1138	2	O84133	(POSSIBLE TRANSMEMBRAN	9.24e+02
833	5	5.0	878	10	Q42704	LIPOKYGENASE 1 (EC 1.1	9.24e+02	906	5	5.0	1140	5	O10028	PUTATIVE GUANYLATE CYC	9.24e+02
834	5	5.0	879	3	Q07807	CHROMOSOME XII READING	9.24e+02	907	5	5.0	1140	11	Q9WV39	DAMAGE-SPECIFIC DNA BI	9.24e+02
835	5	5.0	880	14	Q03820	ENVELOPE POLYPROTEIN G	9.24e+02	908	5	5.0	1142	14	Q9WV39	M POLYPROTEIN.	9.24e+02
836	5	5.0	884	2	Q9XBA6	SENSOR PROTEIN KOPD (F	9.24e+02	909	5	5.0	1144	14	Q9WV39	M POLYPROTEIN.	9.24e+02
837	5	5.0	885	2	Q9X2W8	PPH.	9.24e+02	910	5	5.0	1191	11	P97690	BASMENT MEMBRANE-ASSO	9.24e+02
838	5	5.0	885	3	Q07533	CHROMOSOME IV READING	9.24e+02	911	5	5.0	1194	4	O94965	KIAA0890 PROTEIN.	9.24e+02
839	5	5.0	888	5	Q04135	PUTATIVE RNA-DIRECTED	9.24e+02	912	5	5.0	1203	14	O98815	POL POLYPROTEIN (FRAG	9.24e+02
840	5	5.0	891	1	O93635	STUTTERLYSIN (FRAGMENT	9.24e+02	913	5	5.0	1206	11	O9WTK6	ENDOTHELIAL NITRIC OXI	9.24e+02
841	5	5.0	893	13	Q9W6J4	TRANSCRIPTION FACTOR C	9.24e+02	914	5	5.0	1215	4	O75161	KIAA0673 PROTEIN (FRAG	9.24e+02
842	5	5.0	902	8	Q35063	COXI INTRON1 ORF.	9.24e+02	915	5	5.0	1216	11	O88404	SYNAPTOJANIN 2 ISOFORM	9.24e+02
843	5	5.0	903	5	Q17917	E02H4.3 PROTEIN.	9.24e+02	916	5	5.0	1219	4	O15242	NRD2 CONVERTASE (EC 3.	9.24e+02
844	5	5.0	905	14	P87562	HEXON PROTEIN.	9.24e+02	917	5	5.0	1222	2	O9X349	PX01-79.	9.24e+02
845	5	5.0	914	9	Q9XJB1	PUTATIVE TAIL-HOST SPE	9.24e+02	918	5	5.0	1224	5	O96209	HYPOTHETICAL 144.0 KD	9.24e+02
846	5	5.0	917	14	Q9WS58	REVERSE TRANSCRIPTASE.	9.24e+02	919	5	5.0	1229	11	O35836	NRD2 CONVERTASE (EC 3.	9.24e+02
847	5	5.0	917	14	Q9WI15	POL.	9.24e+02	920	5	5.0	1243	11	O55180	RAT-SLOWPOKE-ALPHA.	9.24e+02
848	5	5.0	917	4	O43444	HEXOKINASE I (EC 2.7.7	9.24e+02	921	5	5.0	1261	5	O45380	RAT-SLOWPOKE-ALPHA.	9.24e+02
849	5	5.0	919	14	Q9WPP0	ENVELOPE GLYCOPROTEIN.	9.24e+02	922	5	5.0	1262	5	O18117	T23F1.5 PROTEIN.	9.24e+02
850	5	5.0	928	2	Q9SG10	PUTATIVE TRANSCRIPTION	9.24e+02	923	5	5.0	1269	10	O22269	PUTATIVE G-BETA-REPEAT	9.24e+02
851	5	5.0	931	10	O04026	HYPOTHETICAL 104.6 KD	9.24e+02	924	5	5.0	1287	5	O26178	GAM1 GENE.	9.24e+02
852	5	5.0	934	1	O73954	DNA TOPOISOMERASE I (F	9.24e+02	925	5	5.0	1287	13	Q91586	MULTIDRUG RESISTANCE P	9.24e+02
853	5	5.0	940	14	O69518	SIMILAR TO MCWV IE2.	9.24e+02	926	5	5.0	1291	2	Q92HU7	VACUOLATING CYTOTOXIN	9.24e+02
854	5	5.0	940	14	O56303	HYPOTHETICAL 107.6 KD	9.24e+02	927	5	5.0	1291	9	O64295	HYPOHETICAL 144.3 KD	9.24e+02
855	5	5.0	941	2	Q92485	110 KDA XYLANASE PRECU	9.24e+02	928	5	5.0	1302	4	O43305	KIAA0421 (FRAGMENT).	9.24e+02
856	5	5.0	948	5	O22155	T04C10.1 PROTEIN.	9.24e+02	929	5	5.0	1308	11	Q922N7	RECEPTOR TYROSINE KINA	9.24e+02
857	5	5.0	949	4	Q9V4E8	KIAA0529 PROTEIN (FRAG	9.24e+02	930	5	5.0	1309	5	O17582	C09H6.1 PROTEIN.	9.24e+02
858	5	5.0	949	10	O41524	SINGLE-SUBUNIT RNA POL	9.24e+02	931	5	5.0	1312	5	O44757	T12F5.4 PROTEIN.	9.24e+02
859	5	5.0	950	13	Q93508	PARAXIAL PROTOCADERIN	9.24e+02	932	5	5.0	1339	5	O26048	BETA-1,3-D-GLUCAN BIND	9.24e+02
860	5	5.0	951	2	O68078	ICE NUCLEAR PROTEIN	9.24e+02	933	5	5.0	1345	14	Q9WT16	MAJOR CAPSID PROTEIN.	9.24e+02
861	5	5.0	954	10	O23437	SIMILARITY TO EXTENSIN	9.24e+02	934	5	5.0	1371	4	O94966	KIAA0891 PROTEIN (FRAG	9.24e+02
862	5	5.0	960	5	O93137	REVERSE TRANSCRIPTASE.	9.24e+02	935	5	5.0	1383	5	O77086	GUANINE NUCLEOTIDE EXC	9.24e+02
863	5	5.0	961	10	O65230	F7N22.14 PROTEIN.	9.24e+02	936	5	5.0	1394	5	O01787	SIMILARITY TO AN AMP-B	9.24e+02
864	5	5.0	961	14	O65661	1A PROTEIN.	9.24e+02	937	5	5.0	1415	5	O94155	UNC-40 (T19B4.6 PROTEI	9.24e+02
865	5	5.0	963	10	Q9XE96	HYPOTHETICAL 106.3 KD	9.24e+02	938	5	5.0	1418	5	O01837	SIMILARITY TO THE CATY	9.24e+02
866	5	5.0	964	5	O10461	HYPOTHETICAL 106.7 KD	9.24e+02	939	5	5.0	1434	2	Q9Y2D6	KIAA0921 PROTEIN (FRAG	9.24e+02
867	5	5.0	964	2	O84877	PUTATIVE OUTER MEMBRAN	9.24e+02	940	5	5.0	1438	2	Q9X7H1	APP PROTEIN.	9.24e+02
868	5	5.0	976	5	O19128	UBIQUITIN-SPECIFIC PRO	9.24e+02	941	5	5.0	1438	14	O96221	WEB-1 ORTHOLOG.. WD40.	9.24e+02
869	5	5.0	981	4	Q9V5B5	COSMIDITIN-SPECIFIC PRO	9.24e+02	942	5	5.0	1457	14	Q9WBO4	RNA-DEPENDENT RNA POLY	9.24e+02
870	5	5.0	982	3	O74773	MSH2 (DNA REPAIR PROTE	9.24e+02	943	5	5.0	1457	14	Q9WJB3	RNA DEPENDENT RNA POLY	9.24e+02
871	5	5.0	984	9	O80102	ENDO-N-ACETYLNEURAMINI	9.24e+02	944	5	5.0	1463	14	Q9XN01	ORF1B POLYPROTEIN (FRA	9.24e+02
872	5	5.0	987	6	O18966	EAG CHANNEL.	9.24e+02	945	5	5.0	1471	5	O18245	C27B7.7 PROTEIN.	9.24e+02
873	5	5.0	988	5	Q22317	T07F10.1 PROTEIN.	9.24e+02	946	5	5.0	1482	11	Q63684	NMDAR2B GLUTAMATE RECE	9.24e+02
874	5	5.0	991	14	Q9VJS1	1A PROTEIN.	9.24e+02	947	5	5.0	1507	11	Q63372	NEUREXIN I-ALPHA PRECU	9.24e+02
875	5	5.0	992	14	O90706	HELICASE.	9.24e+02	948	5	5.0	1525	5	O94137	MULTIDRUG RESISTANCE R	9.24e+02
876	5	5.0	1002	14	Q9YN55	OUTER CAPSID PROTEIN V	9.24e+02	949	5	5.0	1526	11	O55078	DNA TOPOISOMERASE II A	9.24e+02
877	5	5.0	1010	4	Q9S836	MYELOID/LYMPHOID LEUCE	9.24e+02	950	5	5.0	1526	11	O55079	DNA TOPOISOMERASE II A	9.24e+02
878	5	5.0	1011	5	Q24273	NEUROMUSCULIN.	9.24e+02	951	5	5.0	1537	13	Q92072	MODIFICATION METHYLASE	9.24e+02
879	5	5.0	1013	4	O43897	TOLLOID-LIKE PROTEIN.	9.24e+02	952	5	5.0	1539	5	Q19611	SIMILARITY TO PUTATIVE	9.24e+02
880	5	5.0	1013	11	O62381	TOLLOID-LIKE (MAMMALIA	9.24e+02	953	5	5.0	1549	5	O20060	F35G12.8 PROTEIN.	9.24e+02
881	5	5.0	1014	4	O00406	G-PROTEIN-COUPLED RECE	9.24e+02	954	5	5.0	1581	4	Q92614	MYELOBLAST KIAA0216.	9.24e+02
882	5	5.0	1016	4	Q92585	MYELOBLAST KIAA0200.	9.24e+02	955	5	5.0	1581	2	Q92614	MYELOBLAST KIAA0216.	9.24e+02
883	5	5.0	1020	10	Q92V79	F15K9.2 PROTEIN.	9.24e+02	956	5	5.0	1604	3	O14148	HYPOTHETICAL 181.4 KD	9.24e+02
884	5	5.0	1026	10	O49529	PREDICTED PROTEIN.	9.24e+02	957	5	5.0	1614	11	O88883	HYPOTHETICAL 183.1 KD	9.24e+02
885	5	5.0	1029	14	Q9VX00	MUCIN-LIKE PROTEIN.	9.24e+02	958	5	5.0	1614	11	O88883	LOW-DENSITY LIPOPROTEI	9.24e+02
886	5	5.0	1034	3	Q9V7E9	FLO1P-RELATED LECTIN E	9.24e+02	959	5	5.0	1687	11	Q9WUF6	TUBEROUS SCLEROSIS 2 P	9.24e+02
887	5	5.0	1034	5	O17117	M151.4 PROTEIN.	9.24e+02	960	5	5.0	1703	11	Q92019	COLLAGEN ALPHA3(VI) PR	9.24e+02
888	5	5.0	1038	5	O61199	T22B11.5 PROTEIN.	9.24e+02	961	5	5.0	1706	14	O56250	RNA POLYMERASE.	9.24e+02
889	5	5.0	1054	4	O44887	KIAA0793 PROTEIN.	9.24e+02	962	5	5.0	1707	14	Q96806	PUTATIVE REPLICASE.	9.24e+02
890	5	5.0	1058	13	Q91480	ACRIFLOPROTEIN B (FRAG	9.24e+02	963	5	5.0	1732	2	O52050	LYSINE SPECIFIC CYSTEI	9.24e+02
891	5	5.0	1061	2	P73998	ACRIFLOPROTEIN B (FRAG	9.24e+02	964	5	5.0	1740	5	Q23891	ORF1740.	9.24e+02
892	5	5.0	1065	2	P71486	EMBR.	9.24e+02	965	5	5.0	1767	5	O19346	F11C1.5 PROTEIN.	9.24e+02
893	5	5.0	1070	4	Q94938	KIAA0856 PROTEIN (FRAG	9.24e+02	966	5	5.0	1919	3	O42998	HYPOHETICAL 217.7 KD	9.24e+02
894	5	5.0	1082	14	Q9WT34	U30 PROTEIN.	9.24e+02	967	5	5.0	1976	6	O27991	HYPOHETICAL 217.7 KD	9.24e+02
895	5	5.0	1094	4	O15032	KIAA0316.	9.24e+02	968	5	5.0	2098	5	Q25757	NONMUSCLE MYOSIN HEAVY	9.24e+02
896	5	5.0	1095	11	O35867	NEURABIN.	9.24e+02	969	5	5.0	2134	14	Q9YLS4	CTRP.	9.24e+02
											2153	14	Q89709	VIRAL RNA POLYMERASE (9.24e+02


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970 5 5.0 2204 14 Q9WHH6 9.24e+02
971 5 5.0 2215 5 Q22465 9.24e+02
972 5 5.0 2274 11 Q921K7 9.24e+02
973 5 5.0 2282 11 Q61479 DNA BINDING PROTEIN RC
974 5 5.0 2314 11 Q9KVC7 A-KINASE ANCHOR PROTEIN
975 5 5.0 2380 5 Q9E266 HYPOTHETICAL 283.6 KD
976 5 5.0 2460 11 Q64512 PROTEIN-TYROSINE PHOSPH
977 5 5.0 2480 10 Q92PY3 F13A10.9 PROTEIN.
978 5 5.0 2488 5 Q61528 GUANINE NUCLEOTIDE EXC
979 5 5.0 2614 5 Q97054 TALIN HOMOLOGUE.
980 5 5.0 2627 4 Q95973 TELOMERASE-ASSOCIATED
981 5 5.0 2629 11 Q08653 TELOMERASE PROTEIN COM
982 5 5.0 2858 14 Q9WCE9 POLYPROTEIN.
983 5 5.0 2872 11 Q9WUH8 FIBRILLIN-1.
984 5 5.0 2948 5 Q93785 F54B4.1 PROTEIN.
985 5 5.0 3015 14 Q9WPH5 POLYPROTEIN.
986 5 5.0 3016 2 P73590 HYPOTHETICAL 311.5 KD
987 5 5.0 3064 14 Q9WSX7 UL36 PROTEIN.
988 5 5.0 3085 4 Q00183 BRCA2 (FRAGMENT).
989 5 5.0 3300 2 Q06304 HYPOTHETICAL 327.0 KD
990 5 5.0 3394 4 Q9Y6V0 WUGSC:H.DJ0784G16.1 PR
991 5 5.0 3418 4 Q13879 BRCA2 GENE EXON 2 (AND
992 5 5.0 3419 11 Q55147 UTROPHIN.
993 5 5.0 3582 2 Q66069 LICHENYSIN SYNTHETASE
994 5 5.0 3848 5 Q76737 TIPIC.
995 5 5.0 3998 14 Q09710 POLYPROTEIN.
996 5 5.0 3972 2 P73139 HYPOTHETICAL 418.3 KD
997 5 5.0 4005 4 Q13744 ALL-1 PROTEIN.
998 5 5.0 4017 14 Q88508 (PURDUE-115).
999 5 5.0 4152 2 Q9ZHL3 LARGE SUPERNATANT PROT
1000 5 5.0 7829 5 Q18559 SIMILAR TO POLYKETIDE

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ALIGNMENTS

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RESULT 1
ID 077088 PRELIMINARY; PRT; 994 AA.
AC 077088;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE DORSAL B.
CN DL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
SEQUENCE FROM N.A.
RN STRAIN-OREGON R;
RN GROSS I., GEORGE P., OERTEL-BUCHHEIT P., SCHNARR M., REICHHART J.-M.;
RT "Dorsal B, a splice variant of the Drosophila factor Dorsal, is a
RT novel Rel/NF-kB transcription factor."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053614; AAC35296.1; -.
DR HSSP; P19838; INFI.
DR PROSITE; PS01204; REL; 1.
DR PFAM; PF00554; RHD; 1.
DR PRINTS; PR00057; NFKBTNSCPFCT.
SEQUENCE 994 AA; 111523 MW; C0F47A7E CRC32;

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Query Match 7.9%; Score 8; DB 5; Length 994;
Best Local Similarity 100.0%; Pred. No. 1.18e-03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 SSIDNSV 188
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Qy 32 SSIDNSV 39
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RESULT 2 PRELIMINARY; PRT; 100 AA.
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ID Q48425
AC Q48425;
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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE HYPOTHETICAL PROTEIN (FRAGMENT).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
RN [1]
SEQUENCE FROM N.A.
RN STRAIN-ATCC 25955;
RC WILLARD B.L.;
RA Thesis (1994), Chemical Engineering, University of Wisconsin-Madison,
RL USA.
RN [2]
SEQUENCE FROM N.A.
RC STRAIN-ATCC 25955;
RC SKRALY F.A., WILLARD B.L., CAMERON D.C.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U30903; AAA74263.1; -.
DR PFAM; PF00158; sigma54; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 100 AA; 11155 MW; 8B32A9F2 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 LNSVIE 8
Qy 36 LNSVIE 42
|||||

RESULT 3 PRELIMINARY; PRT; 241 AA.
ID 005125
AC 005125;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE MOLYBDENUM-BINDING SUBUNIT OF ABC-TRANSPORT SYSTEM PRECURSOR.
CN MODA.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RC LAQUEYERIE A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X99258; CAA67642.1; -.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 241 AA; 25286 MW; EE3621C1 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 AGSSELA 60
Qy 64 AGSSELA 70
|||||

RESULT 4 PRELIMINARY; PRT; 261 AA.
ID P95157
AC P95157;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE HYPOTHETICAL 26.5 KD PROTEIN.
CN MTCY359.16C.
OS Mycobacterium tuberculosis.

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OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA BROWN D., CHURCHER C.M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=H37RV;
 RC COLE S.T., BARRELL B.G., RAJANDREAM M.A.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=H37RV;
 RC MEDLINE; 96181548.
 RA PHILIP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RL "An integrated map of the genome of the tubercle bacillus,
 Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
 leprae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL; 283859; CAB06130.1; -.
 DR HSSP; P37329; IAMF.
 KW Hypothetical protein.
 SQ SEQUENCE 261 AA; 26576 MW; FC5F6A79 CRC32;
 Query Match 6.9%; Score 7; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 74 AGSSELA 80
 QY 64 AGSSELA 70
 RESULT 5
 ID Q20995 PRELIMINARY; PRT; 263 AA.
 AC Q20995;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE COSMID F58G4.
 GN F58G4.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 C Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THERRY-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RL "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA DU Z., LEIMBAC D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;

RA WATERSTON R.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50309; AAB37061.1; -.
 DR PFAM; PF01461; 7tm_4; 1.
 SQ SEQUENCE 263 AA; 30016 MW; 7C4EFE67 CRC32;
 Query Match 6.9%; Score 7; DB 5; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 32 CRNTOLA 38
 QY 58 CRNTOLA 64
 RESULT 6
 ID Q41176 PRELIMINARY; PRT; 285 AA.
 AC Q41176;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE RIBOSOME-INACTIVATING PROTEIN-RELATED PROTEIN (FRAGMENT).
 OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
 OC Luffa.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92338358.
 RA Li B.Y., RAMAKRISHNAN S.;
 RL "Cloning and expression of a Luffa ribosome-inactivating protein-
 related protein.";
 RL Targeted Diagn. Ther. 7:223-233(1992).
 DR EMBL; S40718; AAB22587.1; -.
 DR HSSP; P04475; LBPR.
 DR MENDEL; I5477; Lufcy; 146; 15477.
 DR PFAM; PF00012; HSP70; 1.
 FT NON_TER 1
 SQ SEQUENCE 285 AA; 30591 MW; DBFD38FC CRC32;
 Query Match 6.9%; Score 7; DB 10; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 21 AIOGSVL 27
 QY 12 AIOGSVL 18
 RESULT 7
 ID Q39254 PRELIMINARY; PRT; 399 AA.
 AC Q39254;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE LOW AFFINITY CALCIUM ANTI-PORTER CAX2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA HIRSCHI K.D., ZHEN R., CUNNINGHAM K.W., REA P.A., FINK G.R.;
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(0).
 DR EMBL; U57412; AAB05914.1; -.

DR MENDEL; 6872; Arath.1296;6872.
SQ SEQUENCE 399 AA; 43630 MW; 98395EE0 CRC32;

Query Match 6.9%; Score 7; DB 10; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 185 AGSELA 191
Qy 64 AGSELA 70
|||||

RESULT 8 PRELIMINARY; PRT; 402 AA.
ID Q9ZLJ6 AC Q9ZLJ6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE POLYNUCLEOTIDE ADENYLITRANSFERASE.
GN PCNB.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J99;
RX MEDLINE; 99120557.
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.,
RA SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G.,
RA TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C.,
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRUST T.J.;
RT "Genomic-sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR ENBL; AE001491; AAD06174.1; -;
SQ SEQUENCE 402 AA; 46425 MW; F4369E21 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 364 LNSVIEN 370
Qy 36 LNSVIEN 42
|||||

RESULT 9 PRELIMINARY; PRT; 440 AA.
ID Q9ZKA2 AC Q9ZKA2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ADENYLOSUCCINATE LYASE.
GN PURB.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J99;
RX MEDLINE; 99120557.
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.,
RA SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G.,
RA TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C.,
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRUST T.J.;
RT "Genomic-sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR ENBL; AE001531; AAD06609.1; -;
DR PROSITE; PS00163; FUMARATE LYASES; 1.
SQ SEQUENCE 440 AA; 49667 MW; 07B43099 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 LNSVIEN 333
Qy 36 LNSVIEN 42
|||||

RESULT 10 PRELIMINARY; PRT; 465 AA.
ID Q9YVR4 AC Q9YVR4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE ORF MSV179 PUTATIVE METALLOPROTEASE, SIMILAR TO MUS MUSCULUS
DE GB:L36244.
GN MSV179.
OS Melanoplus sanguinipes entomopoxvirus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUCSON;
RX MEDLINE; 99102612.
RA AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
RL J. Virol. 73:533-552(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TUCSON;
RA AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF063866; AAC97771.1; -;
KW Protease; Metalloprotease.
SQ SEQUENCE 465 AA; 54288 MW; 3171CDA6 CRC32;

Query Match 6.9%; Score 7; DB 14; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 192 IDLNSVI 198
Qy 34 IDLNSVI 40
|||||

RESULT 11 PRELIMINARY; PRT; 606 AA.
ID Q59675 AC Q59675;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ENDO-BETA-1,4-XYLANASE PRECURSOR (EC 3.2.1.8)
DE (ENDO-1,4-BETA-XYLANASE) (1,4-BETA-D-XYLAN XYLANOHYDROLASE).
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CELLULOSA;
RX MEDLINE; 96077124.
RA MILLWARD-SADLER S.J., DAVIDSON K., HAZLEWOOD G.P., BLACK G.W.,
RA GILBERT H.J., CLARKE J.H.;
RT "Novel cellulose-binding domains, NodB homologues and conserved
RT modular architecture in xylanases from the aerobic soil bacteria
RT Pseudomonas fluorescens subsp. cellulosa and Cellvibrio mixtus.";
RL Biochem. J. 312:39-48(1995).
CC -I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
DR ENBL; Z48928; CAA88764.1; -;
DR HSSP; P14768; ICLX.
DR PFAM; PF00331; Glyco_hydro_10; 1.

DR PRINTS: PR00134; GLHYDRASE10.
KW Signal: Xylan degradation; Hydrolase; Glycosidase.
FT SIGNAL 1 19 POTENTIAL.
CH 20 606
SQ SEQUENCE 606 AA; 64841 MW; 07E3E2F2 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 184 LAGSSEL 190
IIIIIIII
QY 63 LAGSSEL 69

RESULT 12
ID Q92WD9 PRELIMINARY; PRT; 938 AA.
AC Q92WD9;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE F20N2.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA SHINN P., BUEHLER E., DEWAR K., DUNN P., FENG J., KIM C., WALKER M.,
RA CONWAY A.B., CONWAY A.R., KURTZ D., OJI O., SHEN Y.K., TORIUMI M.,
RA VYOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
RA ECKER J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F20N2";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002328; AAC03063.1; --
SQ SEQUENCE 938 AA; 103288 MW; EE7A6D4A CRC32;

Query Match 6.9%; Score 7; DB 10; Length 938;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 AGSSELA 260
IIIIIIII
QY 64 AGSSELA 70

RESULT 13
ID O89119 PRELIMINARY; PRT; 1115 AA.
AC O89119;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE PER3 (FRAGMENT).
GN PER3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA TAKUMI T., TAGUCHI K., MIYAKE S., SAKAKIDA Y., TAKASHIMA N.,
RA MATSUBARA C., MAEBAYASHI Y., OKUMURA K., TAKEKIDA S., YANAMOTO S.,
RA YAGITA K., YAN L., YOUNG M.W., OKAMURA H.;
RT "A light independent oscillatory gene mPer3 in mouse SCN and OVLT";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98372739.
RA TAKUMI T., TAGUCHI K., MIYAKE S., SAKAKIDA Y., TAKASHIMA N.,
RA MATSUBARA C., MAEBAYASHI Y., OKUMURA K., TAKEKIDA S., YANAMOTO S.,
RA YAGITA K., YAN L., YOUNG M.W., OKAMURA H.;
RT "A light-independent oscillatory gene mPer3 in mouse SCN and OVLT";
RL EMBO J. 17:4753-4759(1998).

DR EMBL; AJ007377; CAA07484.1; --
FT EMBL; AB013605; BAA33465.1; --
NON_TER 1115 1115
SQ SEQUENCE 1115 AA; 121041 MW; D894816F CRC32;

Query Match 6.9%; Score 7; DB 11; Length 1115;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 863 AGSSELA 869
IIIIIIII
QY 64 AGSSELA 70

RESULT 14
ID Q92603 PRELIMINARY; PRT; 1152 AA.
AC Q92603;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE KIAA0204 PROTEIN.
GN KIAA0204.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97191544.
RA NAGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAWARABAYASI Y., OHARA O.,
RA TANAKA A., KOTANI H., MIYAJIMA N., NOMURA N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
DR EMBL; D86959; BAA13195.1; --
DR PFAM; PF00069; pkinase; 1.
SQ SEQUENCE 1152 AA; 132796 MW; 4053FC00 CRC32;

Query Match 6.9%; Score 7; DB 4; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 758 TSSIDLN 764
IIIIIIII
QY 31 TSSIDLN 37

RESULT 15
ID O00211 PRELIMINARY; PRT; 1204 AA.
AC O00211;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE HSLK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA YAMADA E., KAMEDA Y., ITOH S., KOHAMA Y., YANAMOTO H., TSUJIKAWA K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB002804; BAA19655.1; --
DR PFAM; PF00069; pkinase; 1.
SQ SEQUENCE 1204 AA; 138995 MW; 7486531D CRC32;

Query Match 6.9%; Score 7; DB 4; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 758 TSSIDLN 764
IIIIIIII
QY 31 TSSIDLN 37

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RESULT 16
ID O85619 PRELIMINARY; PRT; 61 AA.
AC O85619;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE L0012.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EDL933;
RX MEDLINE; 98339885.
RA PERNA N.T., MAYHEW G.F., POSFAI G., ELLIOTT S., DONNENBERG M.S.,
RA KAPER J.B., BLATTNER F.R.;
RT "Molecular evolution of a pathogenicity island from enterohemorrhagic
RT Escherichia coli O157:H7.";
RL Infect. Immun. 66:3810-3817(1998).
EMBL; AF071034; AAC31491.1; -.
SEQUENCE 61 AA; 7286 MW; D92B85CF CRC32;

Query Match 5.9%; Score 6; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 INLDDH 48
QY 85 INLDDH 90

RESULT 17
ID O92440 PRELIMINARY; PRT; 85 AA.
AC O92440;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE ACNPNV ORF76.
OS Bombyx mori nuclear polyhedrosis virus (BmNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T3;
RX MEDLINE; 97329351.
RA KAWITA S.G., MAEDA S.;
RT "Sequencing of the putative DNA helicase-encoding gene of the Bombyx
RT mori nuclear polyhedrosis virus and fine-mapping of a region involved
RT in host range expansion.";
RL Gene 190:173-179(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-T3;
RA GOMI S., MAJIMA K., MAEDA S.;
RT "Sequence analysis of the genome of Bombyx mori
RT nucleopolyhedrovirus.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; L33180; AAC63748.1; -.
SEQUENCE 85 AA; 9582 MW; 5361427C CRC32;

Query Match 5.9%; Score 6; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 NTSSID 85
QY 30 NTSSID 35

RESULT 18
ID O57168 PRELIMINARY; PRT; 91 AA.
AC O57168;

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DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE FRAGMENT OF 28K VIRULENCE FACTOR.
GN MYA007R.
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ANKARA;
RA ANTOINE G., SCHEIFLINGER F., FALKNER F.G., DORNER F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94848; AAB96483.1; -.
SEQUENCE 91 AA; 10637 MW; AA9D4906 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 NTSSID 14
QY 30 NTSSID 35

RESULT 19
ID O23930 PRELIMINARY; PRT; 92 AA.
AC O23930;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31) (FRAGMENT).
GN PPC1 OR PPCB.
OS Flaveria pringlei.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Asterales; Asteraceae;
OC Asteroideae; Helanieae; Flaveria.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LEAF;
RX MEDLINE; 97369366.
RA ERNST K.A., WESTHOFF P.;
RT "The phosphoenolpyruvate carboxylase (ppc) gene family of Flaveria
RT trinervia (C4) and F. pringlei (C3): molecular characterization and
RT trexpression analysis of the ppcB and ppcC genes.";
RL Plant Mol. Biol. 34:427-443(1997).
CC -1- CATALYTIC ACTIVITY: PHOSPHATE + OXALOACETATE = H(2)O +
CC PHOSPHOENOLPYRUVATE + CO(2).
DR EMBL; Z71977; CAA96509.1; -.
DR MENDEL; 24103; Flapr:Ppc1;24103.
DR PFAM; PF00311; PEPcase; 1.
KW Pyruvate; Lyase.
FT NON_TER 92
SQ SEQUENCE 92 AA; 10258 MW; 988E3186 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 GSVLTS 80
QY 15 GSVLTS 20

RESULT 20
ID Q49442 PRELIMINARY; PRT; 94 AA.
AC Q49442;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE UNCERTAIN (FRAGMENT).
OS Mycoplasma genitalium.

```

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-G-37;

RA PETERSON S.N., HU P., BOTT K.F., HUTCHISON C.A.;

RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-G-37;

RA PETERSON S.N.;

RL Thesis (1992). Microbiology and Immunology,

RL University of North Carolina Medical School, USA.

DR EMBL; 001738; AAD10348.1; -

FT NON_TER 94

SQ SEQUENCE 94 AA; 11001 MW; 832863C0 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 94;

Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 NSVIEV 45

|||||

QY 37 NSVIEV 42

|||||

RESULT 21

ID O82254

AC O82254; PRELIMINARY; PRT; 103 AA.

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE PUTATIVE GLUTAREDOXIN.

GN F17A22.26 OR T9J23.3.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

OC Arabidopsis.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA ROUNSLEY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON T.M.,

RA SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.;

RL "Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence.;"

RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,

RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,

RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,

RA FRASER C.M., VENTER J.C.;

RL "Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence.;"

RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC005309; AAC03641.1; -

DR EMBL; AC006072; AAD13692.1; -

DR MENDEL; 32853; Arath; 2723; 32853.

DR MENDEL; 35583; Arath; 2723; 35583.

SQ SEQUENCE 103 AA; 11261 MW; 9089B2A5 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 103;

Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 87 VDSGLK 92

|||||

QY 43 VDSGLK 48

|||||

RESULT 22

ID Q9YEB4

AC Q9YEB4; PRELIMINARY; PRT; 109 AA.

DT 01-NOV-1999 (TRENBLrel. 12, Created)

DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE 109AA LONG HYPOTHETICAL PROTEIN.

GN APE0660.

OS Aeropyrum pernix.

OC Archaea; Crenarchaeota; Aeropyrum.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-K1;

RX MEDLINE; 99310339.

RA KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,

RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,

RA HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,

RA TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,

RA YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,

RA NOMURA N., SAKO Y., KIKUCHI H.;

RT "Complete genome sequence of an aerobic hyper-thermophilic

RT crenarchaeon, Aeropyrum pernix K1.;"

RL DNA Res. 6:83-101(1999).

DR EMBL; AP000060; BAA79632.1; -

SQ SEQUENCE 109 AA; 12078 MW; 6151914F CRC32;

Query Match 5.9%; Score 6; DB 1; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 72 ENVDGS 77

|||||

QY 41 ENVDGS 46

|||||

RESULT 23

ID O86610

AC O86610; PRELIMINARY; PRT; 110 AA.

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)

DE BILF2-PUTATIVE GLYCOPROTEIN [PROMOTER] (FRAGMENT).

GN BILF2.

OS Human herpesvirus 4 (Epstein-Barr virus).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae; Lymphocryptovirus.

RN [1]

RP SEQUENCE FROM N.A.

RA SMITH P.R., CAO Y., KARRAN L., JONES M.D., SNUDDEN D., GRIFFIN B.E.;

RT "Complex nature of the major viral polyadenylated transcripts in

RT Epstein-Barr virus-associated tumors.;"

RL J. Virol. 67:3217-3225(1993).

DR EMBL; S61077; CAB31989.1; -

FT NON_TER 110

SQ SEQUENCE 110 AA; 11611 MW; 82005F0C CRC32;

Query Match 5.9%; Score 6; DB 14; Length 110;

Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 78 TNGGYN 83

|||||

QY 25 TNGGYN 30

|||||

RESULT 24

ID Q22483

AC Q22483; PRELIMINARY; PRT; 139 AA.

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)

DE COSMID T14B4.

GN T14B4.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718;
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKIN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX FAVELLO T.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U50191; AAA91243.1; -;
SQ SEQUENCE 139 AA; 15778 MW; 4F1FC5D9 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 QQFVST 77
QY 78 QQFVST 83
|||||

RESULT 25
ID O15186 PRELIMINARY; PRT; 154 AA.
AC O15186;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE COLLA1 AND PDGFB FUSION TRANSCRIPT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA O'BRIEN K.P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA O'BRIEN K.P.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y08643; CAA69333.1; -;
DR EMBL: Y15920; CAA75880.1; -;
DR EMBL: Y15914; CAA75874.1; -;
DR HSSP: P01127; 1PDG.
DR PFAM: PF00341; PDGF; 1.
FT NON_TER 1 154
FT NON_TER 154 154
SQ SEQUENCE 154 AA; 16512 MW; 6DD0301B CRC32;

Query Match 5.9%; Score 6; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 120 AECKTR 125
QY 71 AECKTR 76
|||||

RESULT 26
ID O65096 PRELIMINARY; PRT; 156 AA.

AC O65096;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ATAF1-LIKE PROTEIN (FRAGMENT).
GN SB29.
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Picea.
RN [1]
RP SEQUENCE FROM N.A.
RA PERRY D.J., BOUSQUET J.;
RL Genetics 0:0-0(1998).
DR EMBL: AF051749; AAC32166.1; -;
DR MENDEL; 28868; Picma; 3421; 28868.
FT NON_TER 1 156
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17489 MW; AIDA6728 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 TCYNSA 19
QY 7 TCYNSA 12
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RESULT 27
ID Q9WVQ6 PRELIMINARY; PRT; 158 AA.
AC Q9WVQ6;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PDGF B (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-APA; TISSUE-KIDNEY;
RC NISHIDA E.;
RT "APA hamsters PDGF B partial cDNA";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB028638; BAA78769.1; -;
DR PROSITE; PS00249; PDGF; 1.
FT NON_TER 1 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17608 MW; C4EB5CC3 CRC32;

Query Match 5.9%; Score 6; DB 11; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 AECKTR 84
QY 71 AECKTR 76
|||||

RESULT 28
ID O70699 PRELIMINARY; PRT; 163 AA.
AC O70699;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 08, Last annotation update)
DE HYPOTHETICAL 17.8 KD PROTEIN.
OS human Calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Calicivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAPPORO-LIKE;
RX MEDLINE: 98336510.


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DE HYPOTHETICAL 20.6 KD PROTEIN.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RA TABATA S.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RX MEDLINE: 97061201.
RA KANeko T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RT DNA Res. 3:109-136(1996).
EMBL: D90911; BAA18072.1; -.
KW Hypothetical protein.
SQ SEQUENCE 178 AA; 20608 MW; 73BB2CFA CRC32;

Query Match 5.9%; Score 6; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 140 SSELAA 145
QY 66 SSELAA 71
|||||

RESULT 34
ID O83736 PRELIMINARY; PRT; 180 AA.
AC O83736;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE PTS SYSTEM, NITROGEN REGULATORY IIA COMPONENT (PTSN-2).
GN TP0755.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RT Science 281:375-388(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE001247; AAC65722.1; -.
DR HSSP: P31222; 1A6J.
DR TIGR: TP0755; -.
SQ SEQUENCE 180 AA; 20428 MW; 1A78EB52 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 180;

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Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 SELAAE 74
QY 67 SELAAE 72
|||||

RESULT 35
ID Q15354 PRELIMINARY; PRT; 185 AA.
AC Q15354;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE C-SIS PROTO-ONCOGENE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CHORIOCARCINOMA;
RX MEDLINE: 95388493.
RA DIRKS R.P.H., ONNEKINK C., JANSEN H.J., DE JONG A., BLOEMERS H.P.J.;
RT "A novel human c-sis mRNA species is transcribed from a promoter in c-
RT sis intron 1 and contains the code for an alternative PDGF B-like
RT protein.";
RT Nucleic Acids Res. 23:2815-2822(1995).
DR EMBL: X83705; CAA58679.1; -.
DR HSSP: P01127; 1PDG.
DR PROSITE: PS00249; PDGF; 1.
DR PFAM: PF00341; PDGF; 1.
FT NON_TER 185
FT FT 185
SQ SEQUENCE 185 AA; 20774 MW; C5FAA883 CRC32;

Query Match 5.9%; Score 6; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 AECKTR 85
QY 71 AECKTR 76
|||||

RESULT 36
ID O27457 PRELIMINARY; PRT; 191 AA.
AC O27457;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE FUCULOSE-1-PHOSPHATE ALDOLASE.
GN MTH1406.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE: 98037514.
RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
RA MCDUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT J. Bacteriol. 179:7135-7155(1997).
RL EMBL: AE000903; AAB85883.1; -.
DR HSSP: P11550; 3FUA.
DR PFAM: PF00596; Aldolase_II; 1.
DR TIGR: TP0755; -.
SQ SEQUENCE 191 AA; 20702 MW; BC8B78DC CRC32;

```

Query Match 5.9%; Score 6; DB 1; Length 191;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 134 ELAAEC 139
 QY 68 ELAAEC 73

RESULT 37
 ID Q65594 PRELIMINARY; PRT; 198 AA.
 AC Q65594;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE W04D2.5 PROTEIN.
 GN VIF.
 OS Bovine immunodeficiency-like virus.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 RN [1]
 RA NADIN-DAVIS S.A., CHANG S.C., ROTH J.A., CARPENTER S.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L04972; AAA42764.1; -;
 SQ SEQUENCE 198 AA; 22836 MW; C545A8B2 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 141 SVLTST 146
 QY 16 SVLTST 21

RESULT 38
 ID Q65591 PRELIMINARY; PRT; 198 AA.
 AC Q65591;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE VIF PROTEIN.
 GN VIF.
 OS Bovine immunodeficiency-like virus.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 RN [1]
 RA NADIN-DAVIS S.A., CHANG S.C., ROTH J.A., CARPENTER S.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L04974; AAA42764.1; -;
 SQ SEQUENCE 198 AA; 22797 MW; F5621CAA CRC32;

Query Match 5.9%; Score 6; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 141 SVLTST 146
 QY 16 SVLTST 21

RESULT 39
 ID Q23155 PRELIMINARY; PRT; 208 AA.
 AC Q23155;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE W04D2.5 PROTEIN.
 GN W04D2.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]

RP SEQUENCE FROM N.A.
 RA LENNARD N.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150719.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; 275552; CAA99938.1; -;
 DR PFAM; PF00411; Ribosomal_S11; 1.
 SQ SEQUENCE 208 AA; 22586 MW; 79CBFB88 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 71 NTSSID 76
 QY 30 NTSSID 35

RESULT 40
 ID Q29613 PRELIMINARY; PRT; 210 AA.
 AC Q29613;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE C-SIS ONCOGENE (PLATELET-DERIVED GROWTH FACTOR).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87146463.
 RA VAN DEN OuwELAND A.M.W., VAN GRONINGEN J.J.M., SCHALKEN J.A.,
 RA VAN NECK H.W., BLOEMERS P.J., VAN DE VEN W.J.M.;
 RL "Genetic organization of the c-sis transcription unit.";
 RN [2]
 RP SEQUENCE OF 1-21 FROM N.A.
 RX MEDLINE; 86120370.
 RA VAN DEN OuwELAND A.M.W., ROEBROEK A.J.M., SCHALKEN J.A.,
 RA CLAESSEN C.A.J., BLOEMERS H.P.J., VAN DE VEN W.J.M.;
 RT "Structure and nucleotide sequence of the 5' region of the human and
 RT feline c-sis proto-oncogenes.";
 RL Nucleic Acids Res. 14:765-778(1986).
 DR EMBL; X06297; CAA29623.1; -;
 DR EMBL; X06298; CAA29623.1; JOINED.
 DR EMBL; X06299; CAA29623.1; JOINED.
 DR EMBL; X06300; CAA29623.1; JOINED.
 DR EMBL; X06301; CAA29623.1; JOINED.
 DR EMBL; X06302; CAA29623.1; JOINED.
 DR EMBL; X03494; CAA27210.1; -;
 DR EMBL; M25358; AAA30817.1; -;
 DR EMBL; M25356; AAA30817.1; JOINED.
 DR EMBL; M25357; AAA30817.1; JOINED.
 DR EMBL; M25353; AAA30817.1; JOINED.
 DR EMBL; M25354; AAA30817.1; JOINED.
 DR EMBL; M25355; AAA30817.1; JOINED.
 DR HSSP; P01127; IPDG.
 DR PROSITE; PS00249; PDGF; 1.
 DR PFAM; PF00341; PDGF; 1.

DR PRINTS: PR00438; GFCYSKNOT.
SQ SEQUENCE 210 AA; 23649 MW; 1579ED72 CRC32;

Query Match 5.9%; Score 6; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 AECCTR 104
|||||
QY 71 AECCTR 76

RESULT 41
ID Q19865 PRELIMINARY; PRT; 219 AA.
AC Q19865;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TRENBLrel. 09, Last annotation update)
DE F28C6.5 PROTEIN.
GN F28C6.5.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.
[1]
RN RP SEQUENCE FROM N.A.
RA BURTON J.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THLERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; Z68315; CAA92671.1; -.
SQ SEQUENCE 219 AA; 24585 MW; 97C9A806 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 SELAAE 118
|||||
QY 67 SELAAE 72

RESULT 42
ID P96667 PRELIMINARY; PRT; 219 AA.
AC P96667;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE YDEJ PROTEIN.
GN YDEJ.
OC Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
[1]
RN RP SEQUENCE FROM N.A.
RA BELLOIN C., AYORA S., EXLEY R., HIRSCHBEIN L., OGASAWARA N.,
RX MEDLINE; 98000887.
RC STRAIN-168;
RA KASAHARA Y., ALONSO J.C., LE HEGARAT F.;
RT "Characterization of an lrp-like (lrpC) gene from Bacillus subtilis.";

Mol. Gen. Genet. 256:63-71(1997).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE; 98044033.
RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
RA GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
RA GUISEPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
RA KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAWA K., OGIWARA A., OUDEGA B., PARK S.H.,
RA PARRO V., POHL T.M., PORTELELLA D., PORMOLLIK S., PRESCOTT A.M.,
RA PRESCAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHE E., ROCHE B., ROSE M., SADAIE Y.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
RA SEKIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDI B.,
RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
RA TAKEUCHI M., TAKAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
RA VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENEGER T.,
RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB001488; BAA19357.1; -.
DR EMBL; Z99106; CAB12329.1; -.
SQ SEQUENCE 219 AA; 24355 MW; E4D588E4 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 143 TQLAGS 148
|||||
QY 61 TQLAGS 66

RESULT 43
ID Q98708 PRELIMINARY; PRT; 225 AA.
AC Q98708;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE V-SIS TRANSFORMING PROTEIN P28.
OS Simian sarcoma virus.
OC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses.
RN RP SEQUENCE FROM N.A.
RX MEDLINE; 82242320.
RA DEVARE S.G., REDDY P.E., LAW J.D., AARONSON S.A.;
RT "Nucleotide sequence analysis of the long terminal repeat of
RT integrated simian sarcoma virus: evolutionary relationship with other
RT mammalian retroviral long terminal repeats.";
RL J. Virol. 42:1108-1113(1982).
RN RP SEQUENCE FROM N.A.

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RX MEDLINE; 82247820.
RA DEVARE S.G., REDDY P.E., ROBBINS K.C., ANDERSEN P.R., TRONICK S.R.,
RA AARONSON S.A.;
RT "Nucleotide sequence of the transforming gene of simian sarcoma
virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3179-3182(1982).
RN [3]
RP SEQUENCE OF 1-36 FROM N.A.
RX MEDLINE; 83067415.
RA ROBBINS K.C., DEVARE S.G., REDDY P.E., AARONSON S.A.;
RT "In vivo identification of the transforming gene product of simian
sarcoma virus.";
RL Science 218:1131-1133(1982).
RN [4]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE; 84106822.
RA DEVARE S.G., SHATZMAN A., ROBBINS K.C., ROSENBERG M., AARONSON S.A.;
RT "Expression of the PDGF-related transforming protein of simian sarcoma
virus in E. coli.";
RL Cell 36:43-49(1984).
DR EMBL; J02396; AAA46814.1; -.
DR HSSP; P01127; LPDG.
DR PFAM; PF00341; PDGF; 1.
SQ SEQUENCE 225 AA; 24347 MW; 41165581 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 ABCKTR 85
QY 71 ABCKTR 76

RESULT 44
ID Q20262 PRELIMINARY; PRT; 232 AA.
AC Q20262;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA CEESM67F.
GN F41C3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA CHISSE S.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U23521; AAC46813.1; -.

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SQ SEQUENCE 232 AA; 26687 MW; 3C5DE33B CRC32;

Query Match 5.9%; Score 6; DB 5; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 KFSQTC 151
QY 3 KFSQTC 8

RESULT 45
ID O49374 PRELIMINARY; PRT; 233 AA.
AC O49374;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE HYPOTHETICAL 25.6 KD PROTEIN.
GN F10N7.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA BEVAN M., KOETTER P., HEMPEL S., ENTIAN K.-D., HOHEISEL J.,
RA MEWES H.W., MAYER K., SCHUELLER C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU ARABIDOPSIS SEQUENCING PROJECT;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021636; CAA16571.1; -.
DR MENDEL; 27479; Arath; 3375; 27479.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 25640 MW; 4C2537BB CRC32;

Query Match 5.9%; Score 6; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 211 SSELAA 216
QY 66 SSELAA 71

RESULT 46
ID O04392 PRELIMINARY; PRT; 240 AA.
AC O04392;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE ALBURNE RIBONUCLEASE (FRAGMENT).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Hordeum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. HIMALAYA;
RA ROGERS J.C., ROGERS S.W.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000939; AAB58718.1; -.
DR MENDEL; 14798; Horvu; 1285; 14798.
DR PROSITE; PS00530; RNASE_T2_1; 1.
DR PROSITE; PS00531; RNASE_T2_2; 1.
DR PFAM; PF00445; ribonuclease_T2; 1.
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 26989 MW; 3CC14846 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 65 ABECKTR 70
|||||
Qy 71 ABECKTR 76

RESULT 47
ID Q85318 PRELIMINARY; PRT; 241 AA.
AC Q85318;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE RING ZINC FINGER-CONTAINING PROTEIN, HOMOLOGUE OF VARIOLA D4.
GN P28.
OS Ectromelia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-MOSCOW;
RA MEDLINE: 94082441.
RA SENKEVICH T.G., KOONIN E.V., BULLER R.M.;
RT "A poxvirus protein with a RING zinc finger motif is of crucial
RT importance for virulence."
RL Virology 198:118-128(1993).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: U01161; AAA16258.1; -;
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFAM: PF00097; 2f-C3HC4; 1.
DR Zinc-finger.
SQ SEQUENCE 241 AA; 28382 MW; 361D7C30 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 NTSSID 14
|||||
Qy 30 NTSSID 35

RESULT 48
ID P87607 PRELIMINARY; PRT; 242 AA.
AC P87607;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE 41KBP FRAGMENT FROM LEFT END OF GENOME.
GN D7R OR C7R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-GRI-90;
RA MEDLINE: 97068532.
RA SAFRONOV P.F., PETROV N.A., RIAZANKINA O.I., TOTMENIN A.V.,
RA SHELKUNOV S.N., SANDAKHCHIEV L.S.;
RT "Genes of a circle of hosts for the cowpox virus."
RL Dokl. Akad. Nauk 349:829-833(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-GRI-90;
RA MEDLINE: 98229462.
RA SHELKUNOV S.N., SAFRONOV P.F., TOTMENIN A.V., PETROV N.A.,
RA RIAZANKINA O.I., GUTOV V.V., KOTWAL G.J.;
RT "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
RT proteins."
RL Virology 243:432-460(1998).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL: X94355; CAA64092.1; -;
DR EMBL: Y11842; CAA72557.1; -;
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFAM: PF00097; 2f-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 242 AA; 28569 MW; 4BD9333D CRC32;

Query Match 5.9%; Score 6; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 NTSSID 14
|||||
Qy 30 NTSSID 35

RESULT 49
ID O80074 PRELIMINARY; PRT; 249 AA.
AC O80074;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ANTI REPRESSOR.
OS bacteriophage phi PVL.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98057870.
RA KANEKO J., KIMURA T., KAWAKAMI Y., TOMITA T., KAMIO Y.;
RT "Panton-valentine leukocidin genes in a phage-like particle isolated
RT from mitomycin C-treated *Staphylococcus aureus* V8 (ATCC 49775).";
RL Biosci. Biotechnol. Biochem. 61:1960-1962(1997).
DR EMBL: AB009866; BAA31909.1; -;
DR SEQUENCE 249 AA; 28536 MW; 057CB5A4 CRC32;

Query Match 5.9%; Score 6; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 SVLTST 65
|||||
Qy 16 SVLTST 21

RESULT 50
ID O24048 PRELIMINARY; PRT; 253 AA.
AC O24048;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TONOPLAST INTRINSIC PROTEIN.
GN MBPY OR TIP.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Caryophyllales; Caryophyllales; Alzooaceae;
OC Mesembryanthemum.
RN [1]
RP SEQUENCE FROM N.A.
RA ISHITANI M., BOHNERT H.J.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MIP FAMILY OF TRANSMEMBRANE CHANNEL
CC PROTEINS.
DR EMBL: U43291; AAB17284.1; -;
DR MENDEL; 26903; Mesembryanthemum; 26903.
DR PROSITE: PS00221; MIP; 1.
DR PFAM: PF00230; MIP; 1.
DR PRINTS: PR00783; MINTRINSCP.
KW Transport; Transmembrane.
SQ SEQUENCE 253 AA; 26080 MW; 617BA59F CRC32;

Query Match 5.9%; Score 6; DB 10; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 QLAGSS 115

Qy 62 QLAGSS 67

RESULT 51

ID Q62891 PRELIMINARY; PRT; 254 AA.

AC Q62891

DT 01-JAN-1998 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE SEC22 HOMOLOG.

GN RSEC22.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

SEQUENCE FROM N.A.

RA STRAIN-SPRAGUE DAWLEY;

RX MEDLINE; 96215028.

RA HAY J.C., HIRLING H., SCHELLER R.H.;

RT "Mammalian vesicle trafficking proteins of the endoplasmic reticulum

RT and Golgi apparatus.";

RL J. Biol. Chem. 271:5671-5679(1996).

DR EMBL; U42209; AAB03367.1; -

DR HSSP; P09012; 201A.

DR PFAM; PF00957; synaptobrevin; 1.

SQ SEQUENCE 254 AA; 28344 MW; E90E8AC4 CRC32;

Query Match

Best Local Similarity 100.0%; Score 6; DB 11; Length 254;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 STKINL 138

Qy 82 STKINL 87

RESULT 52

ID O18439 PRELIMINARY; PRT; 256 AA.

AC O18439;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE DIVERGED SERINE PROTEASE PRECURSOR.

OC Helicoverpa armigera (Cotton bollworm).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

OC Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.

RN [1]

SEQUENCE FROM N.A.

RC TISSUE-MIDGUT;

RX MEDLINE; 98067794.

RA BOWN D.P., WILKINSON H.S., GATEHOUSE J.A.;

RT "Differentially regulated inhibitor-sensitive and insensitive protease

RT genes from the phytophagous insect pest, *Helicoverpa armigera*, are

RT members of complex multigene families.";

RL Insect Biochem. Mol. Biol. 27:625-638(1997).

DR EMBL; Y12274; CAA72953.1; -

DR HSSP; P35049; 1TRY.

DR PFAM; PF00089; trypsin; 1.

KW Signal; Protease.

FT SIGNAL 1 21 POTENTIAL.

SQ SEQUENCE 256 AA; 27321 MW; 869C9029 CRC32;

Query Match

Best Local Similarity 100.0%; Score 6; DB 5; Length 256;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 GSVLTS 56

Qy 111111

Qy 15 GSVLTS 20

RESULT 53

ID O76297 PRELIMINARY; PRT; 257 AA.

AC O76297; O76298; O76299;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

DE ACCESSORY GLAND-SPECIFIC PEPTIDE 26AA (FRAGMENT).

GN ACP26AA.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

RN [1]

SEQUENCE FROM N.A.

RC STRAIN-VARIOUS STRAINS;

RX MEDLINE; 98384843.

RA TSAUR S.-C., TING C.-T., WU C.-I.;

RT "Positive selection driving the evolution of a gene of male

RT reproduction, Acp26Aa, of *Drosophila*. II. Divergence versus

RT polymorphism.";

RL Mol. Biol. Evol. 15:1040-1045(1998).

DR EMBL; AF052470; AAC27995.1; -

DR EMBL; AF052471; AAC27997.1; -

DR EMBL; AF052472; AAC27999.1; -

DR EMBL; AF052473; AAC28001.1; -

DR EMBL; AF052474; AAC28003.1; -

DR EMBL; AF052475; AAC28005.1; -

DR EMBL; AF052476; AAC28007.1; -

DR EMBL; AF052477; AAC28009.1; -

DR EMBL; AF052478; AAC28011.1; -

DR EMBL; AF052479; AAC28013.1; -

DR EMBL; AF052480; AAC28015.1; -

DR EMBL; AF052481; AAC28017.1; -

DR EMBL; AF053250; AAC28790.1; -

DR EMBL; AF053251; AAC28792.1; -

DR EMBL; AF053252; AAC28794.1; -

DR EMBL; AF053253; AAC28796.1; -

DR EMBL; AF053254; AAC28798.1; -

DR EMBL; AF053255; AAC28800.1; -

DR EMBL; AF053256; AAC28802.1; -

DR EMBL; AF053257; AAC28804.1; -

DR EMBL; AF053258; AAC28806.1; -

DR EMBL; AF053259; AAC28808.1; -

DR EMBL; AF053260; AAC28810.1; -

DR EMBL; AF053261; AAC28812.1; -

DR EMBL; AF053262; AAC28814.1; -

DR EMBL; AF053263; AAC28816.1; -

DR EMBL; AF053264; AAC28818.1; -

DR EMBL; AF053265; AAC28820.1; -

DR EMBL; AF053266; AAC28822.1; -

DR EMBL; AF053267; AAC28824.1; -

DR EMBL; AF053268; AAC28826.1; -

DR EMBL; AF053269; AAC28828.1; -

DR EMBL; AF053270; AAC28830.1; -

DR EMBL; AF053271; AAC28832.1; -

DR EMBL; AF053272; AAC28834.1; -

DR EMBL; AF053273; AAC28836.1; -

DR EMBL; AF053274; AAC28838.1; -

DR EMBL; AF053275; AAC28840.1; -

DR EMBL; AF053276; AAC28842.1; -

KW Glycoprotein; Behavior; Polymorphism.

FT NON_TER 1 1

FT VARIANT 12 12

N -> S (IN STRAINS AF2, AF3, AF5, AF7, AF10, AU2, AU4, AU5, AU6, AU8, AU10, NY2, NY3, NY4, NY5, NY7, TW1, TW4, TW5, TW7, TW8 AND TW11)

Q -> K (IN STRAINS AU6, NY1, NY2, NY6, NY8, TW2, TW3, TW4, TW7, TW9 AND TW10).

L -> Q (IN STRAINS AF2, AF7, AU4, NY3, NY5 AND TW11).

FT VARIANT 18 18

FT VARIANT 25 25

FT VARIANT 32 32 S -> G (IN STRAIN NY2).

FT VARIANT 33 33 A -> S (IN STRAIN AU3).

FT VARIANT 37 39 NVP -> SVT (IN STRAIN AU3).

FT VARIANT 39 39 P -> T (IN STRAINS AF2, AF7, AU5, AU9, NY3, NY5, NY7, TW10 AND TW11).

FT VARIANT 49 49 I -> L (IN STRAIN AU3).

FT VARIANT 58 58 D -> G (IN STRAIN AF8).

FT VARIANT 72 72 D -> N (IN STRAINS AU2, AU3, AU8, NY4, TW1, TW5 AND TW8).

FT VARIANT 94 94 N -> S (IN STRAINS AF1, AF2, AF3, AF5, AF6, AF7, AF8, AF9, AF10, AU3, AU4, AU6, AU7, NY2, NY3, NY5, NY6, TW3, TW4, TW6, TW7, TW10 AND TW11).

FT VARIANT 102 102 L -> I (IN STRAINS AF1, AF2, AF3, AF5, AF6, AF7, AF8, AF9, AF10, AU2, AU4, AU6, AU7, AU8, NY2, NY3, NY4, TW1, TW3, TW4, TW5, TW6, TW7, TW8, TW10 AND TW11).

FT VARIANT 165 165 E -> Q (IN STRAINS AU1, AU3 AND AU9).

FT VARIANT 200 200 S -> I (IN STRAINS AU5 AND NY2).

FT VARIANT 205 205 A -> V (IN STRAIN NY2).

FT VARIANT 214 214 R -> K (IN STRAIN TW2).

FT VARIANT 219 219 N -> Y (IN STRAIN TW9).

FT VARIANT 246 246 E -> D (IN STRAINS AF6, AF8, AF9, AU4, TW1 AND TW11).

FT VARIANT 255 255 P -> S (IN STRAINS AF5, AF10, AU5 AND TW10).

FT SEQUENCE 257 AA; 28855 MW; 92837F1D CRC32;

Query Match 5.9%; Score 6; DB 5; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 SSIDLN 94
|||||

Qy 32 SSIDLN 37

RESULT 54
ID P96891 PRELIMINARY; PRT; 261 AA.
AC P96891;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE SIGF.
DE SIGF.
GN SIGF.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RA STRAIN-H37RV;
RA OLIVER K., HARRIS D.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RC STRAIN-H37RV;
RC STRAIN-H37RV;
RC BARRELL B.G., RAJANDREAM M.A.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RC STRAIN-H37RV;
RC MEDLINE; 96181548.
RA PHILLIP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RA "An integrated map of the genome of the tubercle bacillus,
Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium leprae."
RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
DR EMBL; 292771; CAB07069.1; -;
DR PFAM; PF00140; sigma70; 1.
SQ SEQUENCE 261 AA; 28793 MW; EBF9A006 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 145 SELAAE 150
|||||

Qy 67 SELAAE 72

RESULT 55
ID Q50547 PRELIMINARY; PRT; 261 AA.
AC Q50547;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE STRESS RESPONSE/STATIONARY PHASE SIGMA FACTOR.
GN SIGF.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RC MEDLINE; 96181544.
RA DEMAYO J., ZHANG Y., KO C., YOUNG D.B., BISHAI W.R.;
RA "A stationary-phase stress-response sigma factor from Mycobacterium tuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 93:2790-2794(1996).
DR EMBL; U41061; AAC44103.1; -;
DR PFAM; PF00140; sigma70; 1.
SQ SEQUENCE 261 AA; 28779 MW; 5F7C46F1 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 145 SELAAE 150
|||||

Qy 67 SELAAE 72

RESULT 56
ID Q92EP8 PRELIMINARY; PRT; 266 AA.
AC Q92EP8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE 3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11).
GN PANB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RC STRAIN-SBW25;
RC STRAIN-SBW25;
RC RAINNEY P.B.;
RA "Adaptation of Pseudomonas fluorescens to the plant rhizosphere."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RC STRAIN-SBW25;
RC STRAIN-SBW25;
RC RAINNEY P.B., BAILEY M.J.;
RA "Physical and genetic map of the Pseudomonas fluorescens SBW25 chromosome";
RT Mol. Microbiol. 19:521-533(1996).
RN [3]
RC STRAIN-SBW25;
RC STRAIN-SBW25;
RC RAINNEY P.B., HEITHOFF D.M., MAHAN M.J.;
RA "Single-step conjugative cloning of bacterial gene fusions involved in microbe-host interactions.";

RL Mol. Gen. Genet. 256:84-87(1997).
 DR EMBL; AJ130846; CAAL0222.1; -.
 KW Transferase; Methyltransferase.
 SQ SEQUENCE 266 AA; 27969 MW; C3017E41 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 185 SELAAE 190

QY 67 SELAAE 72

RESULT 57
 ID Q52256 PRELIMINARY; PRT; 274 AA.

AC Q52256;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE N-ACETYLmannosamine transferase.
 GN RFBA.

OS Salmonella borreze.
 OC Plasmid pMQ799.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95394842.

RA KEENEYSIDE W.J.; WHITFIELD C.;

RT "Lateral transfer of rfb genes: a mobilizable ColeI-type plasmid carries the rfbO:54 (O:54 antigen biosynthesis) gene cluster from

RT J. Bacteriol. 177:5247-5253(1995)."

RL J. Bacteriol. 177:5247-5253(1995).

DR EMBL; L39794; AAC98401.1; -.

KW Transferase; Plasmid.

SQ SEQUENCE 274 AA; 31799 MW; BA21AE0D CRC32;

Query Match 5.9%; Score 6; DB 2; Length 274;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 170 GGYNTS 175

QY 27 GGYNTS 32

RESULT 58
 ID Q51718 PRELIMINARY; PRT; 278 AA.

AC Q51718;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PHA DEPOLYMERASE PRECURSOR.

GN PHAZ.

OS Pseudomonas fluorescens.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
 OC Pseudomonas.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-DSM 7139;

RX MEDLINE; 95050280.

RA SCHIRMER A.; JENDROSSEK D.;

RT "Molecular characterization of the extracellular poly(3-hydroxyoctanoic acid) [P(3HO)] depolymerase gene of Pseudomonas fluorescens Gk13 and of its gene product."

RT J. Bacteriol. 176:7065-7073(1994).

DR EMBL; U10470; AAA64538.1; -.

KW Signal.

FT SIGNAL.

FT CHAIN 34 278

SQ SEQUENCE 278 AA; 30267 MW; 2C97E460 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 174 GGYNTS 179

QY 27 GGYNTS 32

RESULT 59
 ID O65061 PRELIMINARY; PRT; 281 AA.

AC O65061;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE ATAF1-LIKE PROTEIN (FRAGMENT).

GN SB29.

OS Picea mariana (Black spruce).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC ephyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
 OC Picea.

RN [1]

RP SEQUENCE FROM N.A.

RA PERRY D.J.; BOUSQUET J.;

RL Genetics 0:0-0(1998).

DR EMBL; AF051222; AAC32123.1; -.

DR MENDEL; 28845; Picma; 3421; 28845.

FT NON_TER 1

SQ SEQUENCE 281 AA; 31510 MW; 0B06B236 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 139 TCYN5A 144

QY 7 TCYN5A 12

RESULT 60
 ID Q9Y682 PRELIMINARY; PRT; 282 AA.

AC Q9Y682;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE SEC22 HOMOLOG.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA ZHOU J.; YE M.; FU G.; ZHANG Q.; GUAN Z.; HUANG Q.; XU S.; GU B.;

RA CHEN S.; SHEN Y.; CHEN Z.;

RT "Human Sec 22 homolog gene."

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF100749; AAD43013.1; -.

SQ SEQUENCE 282 AA; 31719 MW; EC2FAC69 CRC32;

Query Match 5.9%; Score 6; DB 4; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 STKINL 138

QY 82 STKINL 87

RESULT 61
 ID O23186 PRELIMINARY; PRT; 284 AA.

AC O23186;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE HEAT SHOCK TRANSCRIPTION FACTOR HSF4.
GN HSF4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA BEVAN M., TERRYN N., VOS P., HEIJNEN L., MEWES H.W., SCHUELLER C.,
RA CHALWATZIS N.:
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU ARABIDOPSIS SEQUENCING PROJECT ESSA;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-GREEN SILIQUES;
RX MEDLINE; 98307340.
F PRAENDL R., HINDERHOFER K., EGGERS-SCHUMACHER G., SCHOEFFL F.;
"HSF3, a new heat shock factor from Arabidopsis thaliana, derepresses
the heat shock response and confers thermotolerance when overexpressed
in transgenic plants.";
RL Mol. Gen. Genet. 258:269-278(1998).
DR EMBL; Z99707; CAB16764.1; -.
DR EMBL; Y14069; CAA74398.1; -.
DR HSP; P22813; IHKS.
DR MENDEL; 25505; Arath;1416;25505.
DR PFAM; PF00447; HSF_DNA-bind; 1.
DR PRINTS; PR00056; HSFDOMAIN.
KW Heat shock.
SQ SEQUENCE 284 AA; 31328 MW; 206AB5DC CRC32;

Query Match 5.9%; Score 6; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 171 SSELAA 176
QY 66 SSELAA 71
|||||

RESULT 62
ID Q96320 PRELIMINARY; PRT; 284 AA.
AC Q96320;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HEAT SHOCK TRANSCRIPTION FACTOR.
GN HSF4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-COLUMBIA; TISSUE=LEAVES, AND STEM;
RA NOVER L., SCHARF K., GAGLIARDI D., VERGNE P., CZARNECKA-VERNER E.,
RA GURLEY W.;
RL Cell Stress and Chaperones 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA; TISSUE=LEAVES, AND STEM;
RA BARROS D., CZARNECKA-VERNER E., YUAN C.X., BALDWIN D., GURLEY W.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U68017; AAC31756.1; -.
DR HSP; P22813; IHKS.
DR MENDEL; 7027; Arath;1416;7027.
DR PFAM; PF00447; HSF_DNA-bind; 1.
DR PRINTS; PR00056; HSFDOMAIN.
KW Heat shock.

SQ SEQUENCE 284 AA; 31397 MW; 2F6634C0 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 171 SSELAA 176
QY 66 SSELAA 71
|||||

RESULT 63
ID O28681 PRELIMINARY; PRT; 286 AA.
AC O28681;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHETICAL 31.5 KD PROTEIN.
GN AFI591.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE; 98049343.
RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBEK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AF000992; AAB89657.1; -.
DR TIGR; AFI591; -.
DR PFAM; PF01402; HTH_4; 1.
KW Hypothetical protein.
SQ SEQUENCE 286 AA; 31519 MW; ACE53FAD CRC32;

Query Match 5.9%; Score 6; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 125 LTSTCE 130
QY 18 LTSTCE 23
|||||

RESULT 64
ID O87560 PRELIMINARY; PRT; 294 AA.
AC O87560;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHETICAL 32.8 KD PROTEIN.
OS Bacillus firmus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OF4;
RA WEI Y., GUFFANTI A.A., KRULWICH T.A.;
RT "Sequence analysis and functional studies of a chromosomal region of
alkaliphilic Bacillus firmus OF4 encoding an ABC-type transporter with
similarity of sequence and Na+ exclusion capacity to the Bacillus
RT subtilis Natab transporter.";

```

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF084104; AAC62419.1; -.
DR PFAM; PF00592; DUF3; 1.
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 32773 MW; 85FE92D3 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 NIDGTL 27
| | | | |
QY 93 NIDGTL 98

RESULT 65
ID Q98251 PRELIMINARY; PRT; 298 AA.
AC Q98251;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MC084L.
GN MC084L.
OS Molluscum contagiosum virus subtype 1 (MCV1), and
OS Molluscum contagiosum virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96325459.
RA SENKEVICH T.G., BUGERT J.J., SISLER J.R., KOONIN E.V., DARAI G.,
RA MOSS B.;
RT "Genome sequence of a human tumorigenic poxvirus: prediction of
RT specific host response-evasion genes.";
RL Science 273:813-816(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA SENKEVICH T.G., BUGERT J.J., SISLER J.R., KOONIN E.V., DARAI G.,
RA MOSS B.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SUBTYPE 1-VARIANT;
RX MEDLINE; 98125989.
RA WATANABE T., MORIKAWA S., SUZUKI K., MIYAMURA T., TAMAKI K., UEDA Y.;
RT "Two major antigenic polypeptides of molluscum contagiosum virus.";
RL J. Infect. Dis. 177:284-292(1998).
RL EMBL; U60315; AAC55212.1; -.
SQ SEQUENCE 298 AA; 32040 MW; 1561F2FD CRC32;

Query Match 5.9%; Score 6; DB 14; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 203 LAGSSE 208
| | | | |
QY 63 LAGSSE 68

RESULT 66
ID Q9Y3Q9 PRELIMINARY; PRT; 306 AA.
AC Q9Y3Q9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE ECTO-ATP DIPHOSPHOHYDROLASE II (EC 3.6.1.5).
GN PLEA 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-PLACENTA;
RA MATSUMOTO M., SAKURAI Y., KOKUBO T., YAGI H., MATSUI T., TITANI K.,
RA FUJIMURA Y., NARITA N.;
RT "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
RT and II.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133134; CAB41887.1; -.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
KW Hydrolase.
SQ SEQUENCE 306 AA; 34175 MW; 2F33C431 CRC32;

Query Match 5.9%; Score 6; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 193 LGKFSQ 198
| | | | |
QY 1 LGKFSQ 6

RESULT 67
ID O60987 PRELIMINARY; PRT; 311 AA.
AC O60987;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE G2-LIKE.
GN G2.
OS Dictyostelium discoideum (Slime mold).
OC Plasmid bdp5.
OC Eukaryota; Dictyostellida; Dictyostelium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WS2162;
RX MEDLINE; 98198836.
RA RIEBEN W.K. JR., GONZALES C.M., GONZALES S.T., PILKINGTON K.J.,
RA KIYOSAWA H., HUGHES J.E., WELKER D.L.;
RT "Dictyostelium discoideum nuclear plasmid bdp5 is a chimera related to
RT the Ddp1 and Ddp2 plasmid families.";
RL Genetics 148:1117-1125(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WS2162;
RA RIEBEN W.K., GONZALES C., GONZALES S.T., PILKINGTON K., KIYOSAWA H.,
RA HUGHES J.E., WELKER D.L.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000580; AAC14394.1; -.
KW Plasmid.
SQ SEQUENCE 311 AA; 36889 MW; 2D354975 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 VSTKIN 115
| | | | |
QY 81 VSTKIN 86

RESULT 68
ID O14047 PRELIMINARY; PRT; 312 AA.
AC O14047;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHETICAL 35.2 KD PROTEIN C2C4.14C IN CHROMOSOME I.
GN SPAC2C4.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-972;
RA OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
    PROTEIN KINASES. STRONGEST TO THE STE20 SUBFAMILY.
DR EMBL; 299259; CAB16374.1; -.
DR PFAM; PF00069; pkinase; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT BINDING 35 35 ATP (BY SIMILARITY).
FT ACT_SITE 127 127 BY SIMILARITY.
SQ SEQUENCE 312 AA; 35218 MW; 7576E17B CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 57 IDLSV 62
OY 34 IDLSV 39
ID 008964 PRELIMINARY; PRT; 313 AA.
AC 008964;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DE 01-AUG-1998 (TRENBLrel. 07, Last annotation update)
DE PROTOCOLADHERIN 5 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA OBATA S., SAGO H., MORI N., DAVIDSON M., ST JOHN T., SHINTARO S.T.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004277; BAA20360.1; -.
FT NON_TER 1
SQ SEQUENCE 313 AA; 33922 MW; F2F03E66 CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 DGLKY 128
OY 95 DGLKY 100
ID 012145 PRELIMINARY; PRT; 317 AA.
AC 012145;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE HYPOTHETICAL 35.4 KD PROTEIN IP012C.
GN IP012C OR LPZ12C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA BADCOCK K., BOWMAN S., CHURCHER C.M., PEARSON D., RAJANDREAM M.A.,
RA WALSH S.V., BARRELL B.G.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AB972;
RA BOWMAN S.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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RC STRAIN-AB972;
RA BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA WANG Y., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D., HALL J.,
RA STORMS R.K., VO D.H., WINNETT E.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86028187.
RA HIEFER P., PRIDMORE D., HEGEMANN J.H., THOMAS M., DAVIS R.W.,
RA PHILIPPSEN P.;
RT "Functional selection and analysis of yeast centromeric DNA.";
RL Cell 42:913-921(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91117242.
RA YANO R., NOMURA M.;
RT "Suppressor analysis of temperature-sensitive mutations of the largest
RT subunit of RNA polymerase I in Saccharomyces cerevisiae: a suppressor
RL gene encodes the second-largest subunit of RNA polymerase I.";
RL Mol. Cell. Biol. 11:754-764(1991).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92371421.
RA GAXIOLA R., DE LARRINOA I.F., VILLALBA J.M., SERRANO R.;
RT "A novel and conserved salt-induced protein is an important
RT determinant of salt tolerance in yeast.";
RL EMBO J. 11:3157-3164(1992).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93156813.
RA MOYA M., ROBERTS D., NOVICK P.;
RT "DSS4-1 is a dominant suppressor of sec4-8 that encodes a nucleotide
RT exchange protein that aids Sec4p function.";
RL Nature 361:460-463(1993).
DR EMBL; Z71255; CAA95009.1; -.
DR EMBL; Z49919; CAA90157.1; -.
DR EMBL; U31900; AAA97591.1; -.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 2.
DR PFAM; PF00096; zf-C2H2; 2.
DR PRINTS; PR00048; ZINC_FINGER.
KW Hypothetical protein; Zinc-finger; Metal-binding; DNA-binding.
SQ SEQUENCE 317 AA; 35358 MW; 5E32D6BE CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 STKINL 74
OY 82 STKINL 87
ID 09Y028 PRELIMINARY; PRT; 324 AA.
AC 09Y028;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE GAG-RELATED PROTEIN (FRAGMENT).
GN ORF3.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TULAHUEN;
RX MEDLINE; 95205412.
RA MARTIN F., MARANON C., OLIVARES M., ALONSO C., LOPEZ M.C.;
RT "Characterization of a non-long terminal repeat retrotransposon cDNA
RT (Ltrc) from Trypanosoma cruzi: homology of the first ORF with the ape
RT family of DNA repair enzymes.";

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RL J. Mol. Biol. 247:49-59(1995).
 DR EMBL; X83098; CAB41694.1; -.
 FT NON_TER 1
 SQ SEQUENCE 324 AA; 36941 MW; DE1604F2 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 324;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 294 LGKFSQ 299
 QY 1 LGKFSQ 6

RESULT 72
 ID O07641 PRELIMINARY; PRT; 327 AA.
 AC O07641;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 GN NIFH.
 OS Nitrogenase reductase.
 OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC51142;
 RA COLON-LOPEZ M., SHERMAN L.A.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003336; AAB61408.1; -.
 DR HSP; P00459; INIP.
 DR PROSITE; PS00692; NIFH_FRXC_2; 1.
 DR PROSITE; PS00746; NIFH_FRXC_1; 1.
 DR PFAM; PF00142; fer4_NifH; 1.
 DR PRINTS; PR00091; NITROGNASEII.
 SQ SEQUENCE 327 AA; 35822 MW; F3315D74 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 QPSNFI 27
 QY 50 QPSNFI 55

RESULT 73
 ID Q09026 PRELIMINARY; PRT; 337 AA.
 AC Q09026;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN).
 GN MOB13.
 OS *Enterococcus oeni* (Leuconostoc oenos).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 OC *Enterococcus*.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-8413;
 RX MEDLINE; 94134826.
 RA FREMAUX C., AIGLE M., LONVAUD-FUNEL A.;
 RT "Sequence analysis of *Leuconostoc oenos* DNA: organization of pLO13, a cryptic plasmid."
 RL Plasmid 30:212-223(1993).
 CC -!- FUNCTION: THE INTERACTION OF THE RSA SITE AND THE PRE PROTEIN MAY NOT ONLY SERVES A FUNCTION IN PLASMID MAINTENANCE, BUT ALSO MAY CONTRIBUTES TO THE DISTRIBUTION OF SMALL ANTIBIOTIC RESISTANCE PLASMIDS AMONG GRAM-POSITIVE BACTERIA.
 CC -!- MISCELLANEOUS: PRE PROTEINS CONTAIN CONSERVED POSITIVELY CHARGED AMINO ACIDS PROBABLY INVOLVED IN THE BINDING OF THE PRE PROTEIN TO THE RSA SITE.

CC -!- SIMILARITY: TO OTHER PRE PROTEINS (FROM PLASMIDS PUB110, PMV158, PE194, PT181, PTB913), IN THEIR N-TERMINAL ONLY.
 DR EMBL; M95954; AAA19673.1; -.
 DR PFAM; PF01076; Mob_Pre; 1.
 KW Plasmid; DNA-binding.
 FT BINDING 113 113 DNA (BY SIMILARITY).
 SQ SEQUENCE 337 AA; 39863 MW; DIC982CE CRC32;

Query Match 5.9%; Score 6; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 233 KINLDD 238
 QY 84 KINLDD 89

RESULT 74
 ID O77146 PRELIMINARY; PRT; 339 AA.
 AC O77146;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE REVERSE TRANSCRIPTASE SJRI (FRAGMENT).
 GN RT.
 OS *Schistosoma japonicum* (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHINESE; TISSUE-MIRACIDIUM;
 RA FAN J., BRINDLEY P.J.;
 RT "Retrosposable elements in the *Schistosoma japonicum* genome."
 RL (In) Tada I., Kojima S., Tsuji M. (eds.);
 RL Proceedings of the 9th international congress of parasitology (ICOPA IX), pp.821-825, Monduzzi Editore, Bologna (1998).
 DR EMBL; AF073333; AAC62955.1; -.
 KW RNA-directed DNA polymerase.
 FT NON_TER 1
 SQ SEQUENCE 339 AA; 39335 MW; 22B00C22 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 IQGSVL 65
 QY 13 IQGSVL 18

RESULT 75
 ID O9YWP5 PRELIMINARY; PRT; 347 AA.
 AC O9YWP5;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE VP7.
 OS *Coltivirus* JKT-7075.
 OC Viruses; dsRNA viruses; Reoviridae; Coltivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JKT-7075;
 RX MEDLINE; 98451335.
 RA ATTOUTI H., CHARREL R.N., BILLOIR F., CANTALOUBE J.F., DE MICCO P., DE LAMBALLERIE X.;
 RT "Comparative sequence analysis of American, European and Asian isolates of viruses in the genus *Coltivirus*."
 RL J. Gen. Virol. 79:0-0(0).
 DR EMBL; AF052023; AAC72050.1; -.
 SQ SEQUENCE 347 AA; 38942 MW; 957291C6 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 347;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 IDLNSV 84

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Qy 34 IDLNSV 39

Search completed: Wed Aug 16 09:57:02 2000
Job time : 54 secs.